


```

RP SEQUENCE FROM N.A. (SHORT FORM).
RC TISSUE-Brain, and Keratinocytes.
RX MEDLINE=94043265; PubMed=8226577;
RA di Marco E., Cutuli N., Guerra L., Canceda R., de Luca M.;
RT "Molecular cloning of trke, a novel trk-related putative tyrosine
RT kinase receptor isolated from normal human keratinocytes and widely
RT expressed by normal human tissues.";
RL J. Biol. Chem. 268:24290-24295(1993).
RN [7]
RP SEQUENCE FROM N.A. (SHORT FORM).
RC TISSUE-Ovary;
RX MEDLINE=95151638; PubMed=7848919;
RA Laval S., Butler R., Shelling A.N., Handy A.M., Poulson R.,
RA Ganesan T.S.;
RT "Isolation and characterization of an epithelial-specific receptor
RT tyrosine kinase from an ovarian cancer cell line.";
RL Cell Growth Differ. 5:1173-1183(1994).
RN [8]
RP SEQUENCE FROM N.A.
RA Shilina S., Tamiya G., Oka A., Inoko H.;
RT "Homo sapiens 2,229,812bp genomic DNA of 6p21.3 HLA class I region.";
RL Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: MAY BE INVOLVED IN CELL-CELL INTERACTIONS AND
CC RECOGNITION.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
CC tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1/CAK I (SHOWN HERE) AND 2/CAK
CC II; ARE PRODUCED BY ALTERNATIVE SPLICING. THEY ONLY DIFFER BY THE
CC ABSENCE OF A 37 RESIDUES SEGMENT.
CC -1- TISSUE SPECIFICITY: EXPRESSED AT LOW LEVELS IN MOST ADULT TISSUES
CC AND IS HIGHEST IN THE BRAIN AND LUNG. ABUNDANT IN BREAST CARCINOMA
CC CELL LINES.
CC -1- DOMAIN: THE GLY/PRO-RICH DOMAINS MAY BE REQUIRED FOR AN UNUSUAL
CC GEOMETRY OF INTERACTION WITH LIGAND OR SUBSTRATES.
CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
CC DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 F5/8 TYPE C DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
CC -1- DATABASE: NAME=PROT, NOTE=CD guide CD167a entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/guide/1986613159.g.htm".
CC CC
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CC or send an email to license@isb-sib.ch).
CC CC
DR EMBL, L11315; AAA02866.1; -
DR EMBL, L20817; AAA18019.1; -
DR EMBL, U48705; AAC50917.1; -
DR EMBL, X948208; CAA66871.1; -
DR EMBL, X99023; CAA66871.1; JOINED.
DR EMBL, X99024; CAA66871.1; JOINED.
DR EMBL, X99025; CAA66871.1; JOINED.
DR EMBL, X99026; CAA66871.1; JOINED.
DR EMBL, X99027; CAA66871.1; JOINED.
DR EMBL, X99028; CAA66871.1; JOINED.
DR EMBL, X99029; CAA66871.1; JOINED.
DR EMBL, X99030; CAA66871.1; JOINED.
DR EMBL, X99031; CAA66871.1; JOINED.
DR EMBL, X99032; CAA66871.1; JOINED.
DR EMBL, X99033; CAA66871.1; JOINED.
DR EMBL, X99034; CAA66871.1; JOINED.
DR EMBL, L57508; AAB05208.1; -
DR EMBL, X74979; CAA52915.1; -
DR EMBL, Z29093; CAA82335.1; -
DR EMBL, AP000511; BAB63318.1; -
DR HSSP, P11362; IFEK.
DR MM, 600408; -

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DR	InterPro:	IPR000719;	Euk_pkinase.
DR	InterPro:	IPR000421;	Fa58_C.
DR	InterPro:	IPR02011;	Receptor_tyr_kin_II.
DR	InterPro:	IPR01245;	Tyr_pkinase.
DR	Pfam:	PF00754;	F5_F8_type_C; 1.
DR	Pfam:	PF00069;	pkinase; 1.
DR	SMART:	SM00231;	Fa58C; 1.
DR	SMART:	SM00219;	TyrcC; 1.
DR	PROSITE:	PS00107;	PROTEIN_KINASE_ATP; FALSE_NEG.
DR	PROSITE:	PS00109;	PROTEIN_KINASE_TYR; 1.
DR	PROSITE:	PS00011;	PROTEIN_KINASE_DOM; 1.
DR	PROSITE:	PS00239;	RECEPTOR_TYR_KIN_II; 1.
DR	PROSITE:	PS01285;	Fa58C_1; 1.
DR	PROSITE:	PS01286;	Fa58C_2; 1.
KW	Transferase:	Tyrosine-protein kinase;	Glycoprotein; signal;
KW	Phosphorylation:	Transmembrane; Receptor; ATP-binding;	Antigen;
KW	Alternative splicing:		
FT	SIGNAL	1	18 POTENTIAL.
FT	CHAIN	19	913 EPITHELIAL DISCOIDIN DOMAIN RECEPTOR 1.
FT	DOMAIN	19	416 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	417	443 POTENTIAL.
FT	DOMAIN	444	913 CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	31	185 F5/F8 TYPE C (PHOSPHOLIPID-BINDING, POTENTIAL)
FT	DOMAIN	377	415 GLY/PRO-RICH.
FT	DOMAIN	476	601 GLY/PRO-RICH.
FT	DOMAIN	610	905 PROTEIN KINASE.
FT	NP_BIND	616	624 ATP (BY SIMILARITY).
FT	BINDING	655	655 ATP (BY SIMILARITY).
FT	ACT_SITE	766	766 BY SIMILARITY.
FT	DISULFID	31	185 BY SIMILARITY.
FT	MOD_RES	513	513 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT	MOD_RES	792	792 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT	MOD_RES	796	796 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT	MOD_RES	797	797 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT	CARBOHYD	211	211 N-LINKED (GLCNAC...) (POTENTIAL).
FT	CARBOHYD	260	260 N-LINKED (GLCNAC...) (POTENTIAL).
FT	CARBOHYD	371	371 N-LINKED (GLCNAC...) (POTENTIAL).
FT	CARBOHYD	394	394 N-LINKED (GLCNAC...) (POTENTIAL).
FT	VARSPLIC	506	542 MISSING (IN ISOFORM 2).
FT	CONFLICT	94	94 L->V (IN REF. 2 AND 3).
FT	CONFLICT	833	833 L->V (IN REF. 2 AND 3).
FT	CONFLICT	847	867 QLTQGVLENGMEFFERDOGR -> SAHRRACHRGEGVLP GGPQA (IN REF. 4).
SEQUENCE	913 AA;	101127 MM;	C96913EA906481E CRC64;
Query Match	Best Local Similarity	99.2%;	Score 4887; DB 1; Length 913;
Matches	913; Conservative	0;	Mismatches 0; Indels 6; Gaps 1.
OY	1	MGPEALSSILLLLLVASGDADMKGHPPDKCYVALGMDORTIPDSISASSMSDSTAR	60
DB	1	MGPEALSSILLLLLVASGDADMKGHPPDKCYVALGMDORTIPDSISASSMSDSTAR	60
OY	61	HSRLSSDGDAWCAGSVFPKKEEYLQVDLRHLVALVGTQGRNAGLGKESRYTL	120
DB	61	HSRLSSDGDAWCAGSVFPKKEEYLQVDLRHLVALVGTQGRNAGLGKESRYTL	120
OY	121	RYSRDGRMMGWKKDMWGQEVISGNDDPEGVVILKDGPMPVARLVRFYPADRVMSYCLAV	180
DB	121	RYSRDGRMMGWKKDMWGQEVISGNDDPEGVVILKDGPMPVARLVRFYPADRVMSYCLAV	180
OY	181	ELYGGLMRDGLLSYAPVGOPTMYLSEAYVLNDSTVDGHTVGGLQGGGLDLADVGGD	240
DB	181	ELYGGLMRDGLLSYAPVGOPTMYLSEAYVLNDSTVDGHTVGGLQGGGLDLADVGGD	240
OY	241	FRKSQELRWPGDYDVGSNNHSSFGSYEMEEFPDLRAFAQMAYHCNMHTLGARLPQG	300
DB	241	FRKSQELRWPGDYDVGSNNHSSFGSYEMEEFPDLRAFAQMAYHCNMHTLGARLPQG	300
OY	301	VECRRRRCPAMAWGEPPRHNLGMLGDPARRAAVSVPJGGVARTLQCFEFAGFWLLFS	360
DB	301	VECRRRRCPAMAWGEPPRHNLGMLGDPARRAAVSVPJGGVARTLQCFEFAGFWLLFS	360

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Db 301 VECFRRCBPAMWEGEPHRLNGNLGDPARAVSVPLGGVARFLQCRFLFAGPMLIFS 360
QY 361 ELSFISDVYNNSSPALGGFPFPPMPMPPPPPPPPPPPPPPPPPPPPPPPPPPPPP 420
Db 361 ELSFISDVYNNSSPALGGFPFPPMPMPPPPPPPPPPPPPPPPPPPPPPPPPPPPP 420
QY 421 GCLVAIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII 480
Db 421 GCLVAIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII 480
QY 481 PPPYQEPFRGPPHSPAPCVNPGSALLSNPAYRLLATYARPGRPGPPPTPMAKPNT 540
Db 481 PPPYQEPFRGPPHSPAPCVNPGSALLSNPAYRLLATYARPGRPGPPPTPMAKPNT 540
QY 541 QAYSGDYMEPEKPGAPLLPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP 600
Db 541 QAYSGDYMEPEKPGAPLLPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP 600
QY 601 PRVDEPRSRRLRFRKEKLEGEQFGEVHLCEVDSPODLVSLDFPLVRKGPPLVAVKILRPD 660
Db 601 PRVDEPRSRRLRFRKEKLEGEQFGEVHLCEVDSPODLVSLDFPLVRKGPPLVAVKILRPD 660
QY 661 ATKNSFSLFSRNDLFKEVKINSRLKDPNIIIRLLGVCVDDPLCMITDYMENGLNQFLS 720
Db 661 ATKNSFSLFSRNDLFKEVKINSRLKDPNIIIRLLGVCVDDPLCMITDYMENGLNQFLS 720
QY 721 AQLQEDKAEAGAPGQQAAGPTISYPMILHYAAQASGKRIATLNFVHRDLATNCLV 780
Db 721 AQLQEDKAEAGAPGQQAAGPTISYPMILHYAAQASGKRIATLNFVHRDLATNCLV 780
QY 781 GENFTIKIDFGMSRLVAGDYRYVQGRAVLPFRMWAMBCILMGKFTTASDVAFVTL 840
Db 781 GENFTIKIDFGMSRLVAGDYRYVQGRAVLPFRMWAMBCILMGKFTTASDVAFVTL 840
QY 841 EYLMLCRAQPFQGLTDEQYIENAGEFFRDQGRQVYLSRRPACPOGLYEILMRCMSRESE 900
Db 841 EYLMLCRAQPFQGLTDEQYIENAGEFFRDQGRQVYLSRRPACPOGLYEILMRCMSRESE 900
QY 901 RPPFSQLHRLMEDALNTV 919
Db 901 RPPFSQLHRLMEDALNTV 919

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CC -1- TISSUE SPECIFICITY: VARIOUS EMBRYONIC AND ADULT TISSUES; ALSO
CC PROLIFERATIVE ZONES OF THE DEVELOPING BRAIN; HIPPOCAMPAL NEURONS.
CC -1- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF TYR-PROTEIN
CC KINASES.
CC -1- SIMILARITY: CONTAINS 1 F5/8 TYPE C DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
CC -----
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DR EMBL: L26525; AAA21089.1; .
DR HSSP: P1362; IAGW.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR000421; FAS8_C.
DR InterPro: IPR002011; Receptor_tyr_kin_II.
DR InterPro: IPR001245; Tyrosine_kinase.
DR Pfam: PF00754; F5_F8_type_C.1.
DR Pfam: PF00069; pkinase.1.
DR SMART: SM00231; FAS8C.1.
DR SMART: SM00219; Tyrc.1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR.1.
DR PROSITE: PS00239; RECEPTOR_TYR_KIN_II.1.
DR PROSITE: PS01285; FAS8C.1.1.
DR PROSITE: PS01286; FAS8C.2.1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM.1.
DR TRANSFERASE: Tyrosine-protein kinase; Glycoprotein; signal;
KW Phosphorylation; Transmembrane; Receptor; ATP-binding.
FT SIGNAL 1 19
FT CHAIN 20 910
FT DOMAIN 20 413
FT TRANSMEM 414 440
FT DOMAIN 441 910
FT DOMAIN 32 186
FT FT 378 412
FT FT 473 598
FT DOMAIN 607 902
FT NP_BIND 613 621
FT BINDING 652 652
FT ACT_SITE 763 763
FT DISULFID 32 186
FT MOD_RES 510 510
FT MOD_RES 789 789
FT MOD_RES 793 793
FT MOD_RES 794 794
FT CARBOHYD 212 212
FT CARBOHYD 261 261
FT CARBOHYD 371 371
FT CARBOHYD 391 391
FT SEQUENCE 910 AA: 101164 MW: 757FAIDBC029806 CRC64;

Query Match 92.9%; Score 4576.5; DB 1; Length 910;
Best Local Similarity 93.0%; Pred. No. 1,7e-234;
Matches 856; Conservative 20; Mismatches 33; Indels 11; Gaps 3;

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QY 180 VELGCLMRDGLSTYAPVGTMTLSAVYINDSTYGHVVGGLQYGLGLADGVGLD 239
DB 181 VELGCLMRDGLSTYAPVGTMTLSAVYINDSTYGHVVGGLQYGLGLADGVGLD 240
QY 240 DEFSQELRWPGDYGVGMSHSFSGYVEKEFEEDRLRAQAQAVCNHNTTGARLPG 299
DB 241 DEFSQELRWPGDYGVGMSHSFSGYVEKEFEEDRLRAQAQAVCNHNTTGARLPG 300
QY 300 GVECFRFRGPAMAMEGEPHRLNGLGDPARAVSVPLGRVAFRCFLFAGPMLLE 359
DB 301 GVECFRFRGPAMAMEGEPHRLNGLGDPARAVSVPLGRVAFRCFLFAGPMLLE 360
QY 360 SEISFISDVYNNSSPALGTFPPAPWMPPGPPPTNFSSLELEPRGQOPVAKAESPTAIL 419
DB 361 SEISFISDVYNNSSPALGTFPPAPWMPPGPPPTNFSSLELEPRGQOPVAKAESPTAIL 416
QY 420 IGCYVAIILLLILALMLRLHRRLLSKAERVYLEELTVLSVGDITLNNRGPGR 479
DB 417 IGCYVAIILLLILALMLRLHRRLLSKAERVYLEELTVLSVGDITLNNRGPGR 476
QY 480 EPPYQEPFRGNPPHSPACVPCNSALLNSPAYRLTLATYARPPRGPPPTPMARKPTN 539
DB 477 EPPYQEPFRGNPPHSPACVPCNSALLNSPAYRLTLATYARPPRGPPPTPMARKPTN 536
QY 540 TQAVSGDYMEPEKRGADLPPPPONSVPYHVAEADIVTLQGTGNTYAVPALPGAVG 599
DB 537 TQAVSGDYMEPEKRGADLPPPPONSVPYHVAEADIVTLQGTGNTYAVPALPGAVG 596
QY 600 PPVDFRSLRLRREKKEGEGFVHLCEYDSQDLYSLDFPLNVRKGHPLVAVKILRP 659
DB 597 PPVDFRSLRLRREKKEGEGFVHLCEYDSQDLYSLDFPLNVRKGHPLVAVKILRP 656
QY 660 DATKNAFSLSFNRDEFLKEVKINSRLKDPNIRLLGYCYODDPLCKMTDYNENGLNOFL 719
DB 657 DATKNAFSLSFNRDEFLKEVKINSRLKDPNIRLLGYCYODDPLCKMTDYNENGLNOFL 710
QY 720 SAHQLEKAAEGAPGDAQAGPTISTPMLLHVAQAQIASMRVLTATNFVHRDLATNCL 779
DB 711 SAHQLEKAAEGAPGDAQAGPTISTPMLLHVAQAQIASMRVLTATNFVHRDLATNCL 770
QY 780 VGENFTIKINDFGMSRLLYAGDYRNOGRAVLPILRMAMACILMGKTTASDVMAFVTL 839
DB 771 VGENFTIKINDFGMSRLLYAGDYRNOGRAVLPILRMAMACILMGKTTASDVMAFVTL 830
QY 840 MEYLMCLRAOPFQGLTDEQYIENAGEFFRDGROVYLSRPACPOGLYELMLCKMSHSE 899
DB 831 MEYLMCLRAOPFQGLTDEQYIENAGEFFRDGROVYLSRPACPOGLYELMLCKMSHSE 890
QY 900 QRPFFSOLHFFLAEDALNTV 919
DB 891 QRPFFSOLHFFLAEDALNTV 910

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RX MEDLINE-96204002; PubMed-8622863;
RA Perez J.L., Jing S.O., Wong T.W.;
RT "Identification of two isoforms of the Cak receptor kinase that are
RL coexpressed in breast tumor cell lines.";
RN Oncogene 12:1469-1477(1996).
[2]
RC SEQUENCE OF 766-822 FROM N.A.
RP STRAIN-C57BL; TISSUE-Embryonic brain;
RX MEDLINE-9306484; PubMed-1281307;
RA Gallard-Hebenstreit P., Nieto M.A., Fraim M., Mattei M.-G.,
RA Chester A., Wilkinson D.G., Charney P.;
RT "An Eph-related receptor protein tyrosine kinase gene segmentally
RT expressed in the developing mouse hindbrain.";
RL Oncogene 7:2499-2506(1992).
CC -1- FUNCTION: MAY BE INVOLVED IN CELL-CELL INTERACTIONS AND
CC RECOGNITION (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
CC tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: CAK I (SHOWN HERE) AND CAK II;
CC ARE PRODUCED BY ALTERNATIVE SPLICING. THEY ONLY DIFFER BY THE
CC ABSENCE OF A 37 RESIDUES SEGMENT.
CC -1- TISSUE SPECIFICITY: THE PREDOMINANT ISOFORM CAK I, IS EXPRESSED IN
CC DEVELOPING EMBRYO AND ADULT BRAIN; CAK II IS EXPRESSED IN VARIOUS
CC EPITHELIAL CELLS.
CC -1- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF TYR-PROTEIN
CC KINASES.
CC -1- SIMILARITY: CONTAINS 1 F5/8 TYPE C DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
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DR EMBL: L57509; AAB05209.1; -
DR EMBL: X57240; CAA0516.1; -
DR PIR: S30502; S30502.
DR HSSP: P11362; IAGW.
DR MGD: MGI:99216; Ddrl.
DR InterPro: IPR000719; Euk_Pkinase.
DR InterPro: IPR000421; FA5B_C.
DR InterPro: IPR002011; Receptor_tyr_kin_II.
DR InterPro: IPR001245; Tyr_Pkinase.
DR Pfam: PF00754; F5_F8_Tyr_C; 1.
DR SMART: SM00231; FA58C; 1.
DR SMART: SM00219; TyrKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00239; RECEPTOR_TYR_KIN_II; 1.
DR PROSITE: PS01285; FA58C_1; 1.
DR PROSITE: PS01286; FA58C_2; 1.
KW Transferase; Tyrosine-protein kinase; Glycoprotein; Signal;
KW Phosphorylation; Transmembrane; Receptor; ATP-binding;
KW Alternative splicing.
FT SIGNAL 1 19
FT CHAIN 20 911
FT DOMAIN 20 414
FT TRANSMEM 415 441
FT DOMAIN 442 911
FT DOMAIN 32 186
FT DOMAIN 379 413
FT DOMAIN 474 599
FT DOMAIN 608 903
FT NP_BIND 614 622
FT BINDING 653 653

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FT	ACT_SITE	764	764	BY SIMILARITY.
FT	DISULFID	32	166	BY SIMILARITY.
FT	MOD_RES	511	511	PHOSPHORYLATION (AUTO-) (BY SIMILARITY)
FT	MOD_RES	760	730	PHOSPHORYLATION (AUTO-) (BY SIMILARITY)
FT	MOD_RES	794	794	PHOSPHORYLATION (AUTO-) (BY SIMILARITY)
FT	MOD_RES	795	795	PHOSPHORYLATION (AUTO-) (BY SIMILARITY)
FT	CARBOHYD	213	213	N-LINKED (GLCNAc. . .) (POTENTIAL)
FT	CARBOHYD	262	262	N-LINKED (GLCNAc. . .) (POTENTIAL)
FT	CARBOHYD	372	372	N-LINKED (GLCNAc. . .) (POTENTIAL)
FT	CARBOHYD	392	392	N-LINKED (GLCNAc. . .) (POTENTIAL)
FT	VARSPLIC	503	539	N-LINKED (GLCNAc. . .) (POTENTIAL)
1 SQ	SEQUENCE	911 AA:	101160 MM;	MISSING (IN ISOPORN CAK II).

Query Match.	Best Local Similarity	92.5%	Score 4560;	DB 1	Length 911;
Matches 855;	Conservative	20;	Mismatches 34;	Indels 12;	Gaps 4
QY 1	MGPEALSS-L	LLLLLLVASGDADMKGHFDPKACRYALGMDRTIPDSIDASSMSDSTAA	59		
DB 1	MGSGTSL	LLLLLLLLLVITGIDADMKGHFDPKACRYALGMDRTIPDSIDASSMSDSTAA	60		
QY 60	RHSRLSSDDGAMC	AGSAYFKEEETLYVDLQRLHVALYGTGQHAGGLCKESRSR	119		
DB 61	RHSRLSSDDGAMC	AGSAYFKEEETLYVDLQRLHVALYGTGQHAGGLCKESRSR	120		
QY 120	LRSYRGRMRMGKMD	MGOEVLISGNDDPEGVYLKDLGPRMVALYFYPRADVMSYCR	179		
DB 121	LRSYRGRMRMGKMD	KRMGOEVLISGNDDPEGVYLKDLGPRMVALYFYPRADVMSYCR	180		
QY 180	VELYGLMDRLG	LLSTYAPVQGYLYSEA-VYLNDSTYDGHVNGLOLGYGLGOLADGVGL	238		
DB 181	VELYGLMDRLG	LLSTYAPVQGYLYSEA-VYLNDSTYDGHVNGLOLGYGLGOLADGVGL	240		
QY 239	DDEPRKQELRW	MPGYDYVGMNSHFSGGYVEMFEEDRLRAFOAMOVHNNHHTTGARLP	298		
DB 241	DDEPRKQELRW	MPGYDYVGMNSHFSGGYVEMFEEDRLRTQYMOVHNNHHTTGARLP	300		
QY 299	GGYECCFRRG	PAMAMWGEFMRHNLGNLGDPRARAVSVPLGGRVAFLOCRFLFAGPMLL	358		
DB 301	GGYECCFRRG	PAMAMWGEFMRHNLGNLGDPRARAVSVPLGGRVAFLOCRFLFAGPMLL	360		
QY 359	FSEISFISDV	NVNNSPALGTFPPAPAMWPGCPPTMFSELLEPRGOQVAAAEASPTAI	418		
DB 361	FSEISFISDV	NDS-----DTEPPAPAMWPGCPPTMFSELLEPRGOQVAAAEASPTAI	416		
QY 419	LIGCLVAII	LLLLLLIITALMLRMRLHMRLLSKAERYLEBELTVHLSVPGDTILINRRPG	478		
DB 417	LIGCLVAII	LLLLLLIITALMLRMRLHMRLLSKAERYLEBELTVHLSVPGDTILINRRPG	476		
QY 479	REPPROEPR	PGNPNHSAPCVYNGSALLSNPATRLIATYARPRKPGPPTPMAPKT	538		
DB 477	REPPROEPR	PGNPNHSAPCVYNGSALLSNPATRLIATYARPRKPGPPTPMAPKT	536		
QY 539	NTQAYS	SGDIYMEPEKDGAPLPPPONSVPHYAEADIVTLOGVTGGNTYAAVPLPRGAGD	598		
DB 537	NTQAYS	SGDIYMEPEKDGAPLPPPONSVPHYAEADIVTLOGVTGGNTYAAVPLPRGAGD	596		
QY 599	GERPRD	FPSSRLRFKEKLGEGOFGEVHLCEVDSPODLVSLDFPLNVRKGHPLLYAVKILR	658		
DB 597	GERPRD	FPSSRLRFKEKLGEGOFGEVHLCEVDSPODLVSLDFPLNVRKGHPLLYAVKILR	656		
QY 659	PATKNA	SFLFSRNDPLFKEVIMSRLDPNITRLGVCYODDPICMTIDWENDDLOF	718		
DB 657	PATKNA	-----RNDPLFKEVIMSRLDPNITRLGVCYODDPICMTIDWENDDLOF	710		
QY 719	LSAHL	EDKAAEGADGQAAGPTISYPMILHVAQAISAGMYLATLNFVHRLATRNC	778		
DB 711	LSAHL	EDKAAEGADGQAAGPTISYPMILHVAQAISAGMYLATLNFVHRLATRNC	770		
QY 779	LYGNEFT	IKIADFGSRNULYAGDYRYRGGRAVLPTRMMAMCEILMGKTTASDVMAEYVT	838		
DB 771	LYGNEFT	IKIADFGSRNULYAGDYRYRGGRAVLPTRMMAMCEILMGKTTASDVMAEYVT	830		

QY	LMETVLMCRAPFCQGLTDEQYIENNAEGEPPROGQVYLSRPACPOGLYTELMRCMRES	839
Dd	LMETVLMCRSQPFQGLTDEQYIENNAEGEPPROGQVYLSRPACPOGLYTELMRCMREP <td>831</td>	831
QY	EORPEFSQIHRFLADDAINTY	919
Dd	EORPEFSQIHRFLADDAINTY	911

RESULT	4
DDRR_HUMAN	STANDARD; PRT; 855 AA.
ID	DDRR_HUMAN
AC	Q16832;
DT	01-NOV-1997 (Rel. 35, Created)
DT	01-NOV-1997 (Rel. 35, last sequence update)
DT	16-OCT-2001 (Rel. 40, last annotation update)
DE	Discoidin domain receptor 2 precursor (BC 2.7.1.112) (receptor protein-tyrosine kinase TKT) (tyrosine-protein kinase TYRO 10) (neurotrophic tyrosine kinase, receptor-related 3).
DE	DDRR OR NTRK3 OR TKT OR TYRO10.
GN	Homo sapiens (Human).
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Heart, and Thymus;
RX	MEDLINE=94067796; PubMed=82457548;
RA	Karn T., Holtlich U., Braeuninger A., Boehme B., Wolf G., Raebgaumen-Waigman H., Strebhardt K.;
RT	Structure, expression and chromosomal mapping of TKT from man and mouse: a new subclass of receptor tyrosine kinases with a factor VIII-like domain.";
RL	Oncogene 8:3433-3440(1993)
CC	-1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein tyrosine phosphate.
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.
CC	-1- ALTERNATIVE PRODUCTS: DIFFERENT TRANSCRIPTS ARE DERIVED FROM ONE GENE.
CC	-1- TISSUE SPECIFICITY: THE MAJOR 10 kb TRANSCRIPT IS EXPRESSED IN HIGH LEVELS IN HEART AND LUNG, LESS IN BRAIN, PLACENTA, LIVER, SKELETAL MUSCLE, PANCREAS, AND KIDNEY.
CC	-1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN.
CC	-1- SIMILARITY: CONTAINS 1 F5/8 TYPE C DOMAIN.
CC	-1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-PROTEIN KINASES.
CC	-----
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CC	or send an email to license@isb-sib.ch .
CC	-----
CC	EMBL; X74764; CAA52777.1; -.
CC	HSSP; P11362; IACM.
DR	MM; 191311;
DR	InterPro; IPR000719; Euk_Pkinase.
DR	InterPro; IPR000421; FAS5_C.
DR	InterPro; IPR002011; Receptor_tyr_kin_II.
DR	InterPro; IPR001245; Tyr_Pkinase.
DR	Pfam; PF00754; F5_F8_type_C; 1.
DR	Pfam; PF00069; Pkinase; 1.
DR	SMART; SM00231; FAS5C; 1.
DR	SMART; SM00219; TYKIC; 1.
DR	PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR	PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
DR	PROSITE; PS01285; FAS5C_1; 1.
DR	PROSITE; PS01286; FAS5C_2; 1.
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

KM Transferase; Tyrosine-protein kinase; Glycoprotein; Signal;
 KM Phosphorylation; Transmembrane; Receptor; ATP-binding.
 FT SIGNAL 1 21
 FT CHAIN 22 855
 FT DOMAIN 22 399
 FT TRANSHEM 400 421
 FT DOMAIN 422 855
 FT DOMAIN 30 185
 FT DOMAIN 563 849
 FT NP_BIND 569 577
 FT BINDING 608 608
 FT ACT_SITE 710 710
 FT DISULFID 30 185
 FT MOD_RES 740 740
 FT CARBOHYD 121 121
 FT CARBOHYD 213 213
 FT CARBOHYD 261 261
 FT CARBOHYD 280 280
 FT CARBOHYD 372 372
 FT SEQUENCE 855 AA; 96752 MW; D5270BCFD7FED7E CRC64;

Query Match 48.88; Score 2404; DB 1; Length 855;
 Best Local Similarity 51.88; Pred. No. 5.9e-120;
 Matches 482; Conservative 118; Mismatches 227; Indels 104; Gaps 16;

QY 3 PEALSLILLLVASGDADMGHPDPAKCRALGMDRTIPDSISASSWSDTAARHS 62
 DB 5 PRLMLVLFLLPILS---SAKAQVNPALCRPLGMSGGQIDDEDITASSQSESTAAATG 61
 QY 63 RLSSDDGACMPAGSVFPEKE-EELYQVLDLRLHLVALVGTGGHAGLGKFEFSRYLR 121
 DB 62 RLDSSEGGACMPPEIPVPEDDLKEFLQIDLHTLHRTLVGTGGHAGLGIEFAPMYKIN 121
 QY 122 YSPGRRMGKMDRKGQVIGSNGDEBQVVLKDGPRVAVLVPRADVMSCLEAVE 181
 DB 122 YSRDSTRMISRNRRGKVLGNSNPIDIFLKLDEPPIVAFVRIPTDHSNMVCMVEE 181
 QY 182 LYGLMDRGLSYTAPVQGTMYL--SEAVYLNDSTYDGHVGGLOYGGLQGLADGVVLD 239
 DB 182 LYGCWMDGLVSYNAPAGQFVLPGGSIYLDNDYDQ-ANGYMTBELGLTGCVSGLD 240
 QY 240 DFRSQELRVMPGIDYVGMSSHSFSGVTEMEFEFRLRAFQAMOVHNNHTLGARLPG 299
 DB 241 DFTQHEHYVMPGIDYVGMSSHSFSGVTEMEFEFRLRAFQAMOVHNNHTLGARLPG 300
 QY 300 GVEGCFRRGPAMAGEEPMRNHNGNLGDPRAVSVLGLRVARFLQCRFLFAGPWLLE 359
 DB 301 EYQCTF-RSEASEMPPNALSFPVLVDVNPASRFTVPLHHRMASALICQYHFADTWMF 359
 QY 360 SEISFISD-VVNNSSPALGTFPPAPWMPGPPTNFSLELEPRGOQPVAKAEGSPYAI 418
 DB 360 SEIFQSDAPVYNNSEAL---PTSP-----MAPTYDPMKAVDSDNRI 400
 QY 419 LIGCLVALIILLLIILALMLRRLLSKAERVLEELTVLHSPVGGTILNNR--P 476
 DB 401 LIGCLVALIILLLIILALMLRRLLSKAERVLEELTVLHSPVGGTILNNR--P 476
 QY 477 GPRP-----PRYOEPKRGNGNPPHSAFCVNGSALLNSPAYLLATYAR 523
 DB 461 SPSEGGNSTDRIFPLPQYEP-----SRLRKLPDEF----- 494
 QY 524 PRGPGPTPAMAKPTNTQAVSGDMEPEKPGAPLLPPPPONSVHYAEADIVTLQGVYG 583
 DB 495 -----APGEESGSGSVYKVPQSGP-----EGVHYHAEADIVNLOGVYGG 535
 QY 584 NTYAVPALPQAVGDGPRV-DPRSRRLRREKLGEGQFGVHLCEVDSPQDLYSLDFPL 642
 DB 536 NTYSPATYMDLISGKDVAAVEEPRKLLTEFEKLGEGQFGVHLCEVEGMEKFRDXFAL 595
 QY 643 NVRGHPLLVAVKILRPDATKNASFLSRNDELKEVINSRLKDPNITILGVCVQDDP 702
 DB 596 DVSANQVLAVALKRLADANKNA-----RNDPLKEIKIMSRLKDPNITILGVCITDDP 649

QY 703 LCMITDYENGDLNLOFLSAHQLEDKAAGAPDGOAAGPRTISYPMILLHVAQIASGMRY 762
 DB 650 LCMITEYENGDLNLOFLSRHE-----PNNSSSDVRYSTYNLFMAQTQIASGMRY 700
 QY 763 LATNFVHRDLATRNCLVGENFTIKIADFGMSRNLYAGDYRVQRAVLPIRMAMECIL 822
 DB 701 LSLNLFVRDLATRNCLVGENFTIKIADFGMSRNLYAGDYRVQRAVLPIRMAMECIL 760
 QY 823 MKEFTTADVAFAFCTLWEVLMCRAPPGQILTDEQVLENAGEFFRDGROYLSRPPAC 882
 DB 761 LKFTTADVAFAFCTLWEVLMCRAPPGQILTDEQVLENAGEFFRDGROYLSRPPAC 820
 QY 883 POGYEMLRCMSRSEQRPPEPOLHRELA 913
 DB 821 PDSYKMLSCMRDTPKRPSPQETHLILLQ 851

RESULT 5
 DDB2_MOUSE
 ID DDB2_MOUSE STANDARD; PRT: 854 AA.
 AC 062371.
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Discoidin domain receptor 2 precursor (BC 2.7.1.112) (Receptor
 DE protein-tyrosine kinase TKT) (Tyrosine-protein kinase TYRO 10)
 DE (Neurotrophic tyrosine kinase; receptor-related 3).
 GN DDB2 OR NTKR3 OR TKT OR TYRO10.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RX [1]
 RP SEQUENCE FROM N. A.
 RX MEDLINE=94067796; PubMed=8247548;
 RA Kan T., Holtrich U., Braeuninger A., Boehme B., Wolf G.,
 RA Rubsamen-Waigmann H., Streibhardt K.;
 RT "Structure, expression and chromosomal mapping of TKT from man and
 RT mouse: a new subclass of receptor tyrosine kinases with a factor
 RT VIII-like domain.";
 RL Oncogene 8:3433-3440(1993).
 [2]
 RP SEQUENCE FROM N. A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=94151011; PubMed=8108131;
 RA Lal C., Lemke G.E.;
 RT "Structure and expression of the Tyro 10 receptor tyrosine kinase.";
 RL Oncogene 9:877-883(1994).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: DIFFERENT TRANSCRIPTS ARE DERIVED FROM ONE
 CC GENE.
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED; HIGH LEVELS IN SKELETAL
 CC MUSCLE, HEART, CNS, AND KIDNEY; LESS IN OTHER TISSUES. THE MAJOR
 CC 10 KDa TRANSCRIPT IS EXPRESSED IN HIGH LEVELS IN HEART AND LUNG,
 CC LESS IN BRAIN AND TESTIS.
 CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
 CC DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 F5/8 TYPE C DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
 CC PROTEIN KINASES.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X76505; CAA54040.1; ALT_INIT.

CC NEUROTROPHIN-3 AND NEUROTROPHIN-4/5 BUT NOT NERVE GROWTH FACTOR
CC (NGF). INVOLVED IN THE DEVELOPMENT AND/OR MAINTENANCE OF THE
CC NERVOUS SYSTEM. THIS IS A TYROSINE-PROTEIN KINASE RECEPTOR. KNOWN
CC SUBSTRATES FOR THE TRK RECEPTORS ARE SHC, PI-3 KINASE, AND PLC-
CC GAMMA-1.
CC
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
CC tyrosine phosphate.
CC
CC -1- SUBUNIT: EXISTS IN A DYNAMIC EQUILIBRIUM BETWEEN MONOMERIC (LOW
CC AFFINITY) AND DIMERIC (HIGH AFFINITY) STRUCTURES.
CC
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC
CC -1- ALTERNATIVE PRODUCTS: AT LEAST THREE FORMS ARE PRODUCED BY
CC ALTERNATIVE SPLICING; THESE ARE: GP145-TRKB, T1 (GP95-TRKB) AND
CC T2.
CC
CC -1- TISSUE SPECIFICITY: THE DIFFERENT FORMS ARE DIFFERENTIALLY
CC EXPRESSED IN VARIOUS CELL TYPES. THE T2 ISOFORM IS PRIMARILY
CC EXPRESSED IN NEURONS.
CC
CC -1- PFM: LIGAND-MEDIATED AUTO-PHOSPHORYLATION.
CC
CC -1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES. TRK-TYPE SUBFAMILY.
CC
CC -1- SIMILARITY: CONTAINS 2 LEUCINE-RICH REPEATS (LRR).
CC
CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC
CC
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CC or send an email to license@isb-sib.ch).
CC
CC
CC EMBL: M33385; AAA0482.1; -
CC EMBL: X17647; CA353636.1; -
CC PIR: S06943; S06943.
CC PIR: A35104; A35104.
CC HSP: P11362; IFGK.
CC MGD: MG1:97384; NTRK2.
CC
CC InterPro: IPR000719; Euk_Pkinase.
CC InterPro: IPR003006; Ig_MHC.
CC InterPro: IPR003598; Ig_C2.
CC InterPro: IPR001611; LRR.
CC InterPro: IPR000483; LRR_Cterm.
CC InterPro: IPR000372; LRR_Nterm.
CC InterPro: IPR002011; Receptor_Tyr_Kin_II.
CC InterPro: IPR001245; Tyr_Pkinase.
CC
CC Pfam: PF00047; Ig; 1.
CC Pfam: PF00560; LRR; 1.
CC Pfam: PF01463; LRRCT; 1.
CC Pfam: PF01462; LRRNT; 1.
CC Pfam: PF00069; pkinase; 1.
CC PRINTS: PR00109; TYRKINASE.
CC SMART: SM00408; IGC2; 1.
CC SMART: SM00082; LRRCT; 1.
CC SMART: SM00013; LRRNT; 1.
CC SMART: SM00219; TYKIC; 1.
CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
CC PROSITE: PS00239; RECEPTOR_TYR_KIN_II; 1.
CC PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
CC Transferrase: Tyrosine-protein kinase; Transmembrane; ATP-binding;
CC Phosphorylation; Receptor; Glycoprotein; Neurogenesis; Signal;
CC Leucine-rich repeat; Repeat; Immunoglobulin domain.
CC
CC Alternative splicing.
CC
CC FT CHAIN 32 429 BDNF/NT-3 GROWTH FACTORS RECEPTOR.
CC FT DOMAIN 32 429 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 430 453 POTENTIAL.
CC FT DOMAIN 454 821 CYTOPLASMIC (POTENTIAL).
CC FT REPEAT 72 93 LRR 1.
CC FT REPEAT 96 117 LRR 2.
CC FT DOMAIN 214 270 IG-LIKE C2-TYPE DOMAIN 1.
CC FT DOMAIN 301 365 IG-LIKE C2-TYPE DOMAIN 2.
CC FT DOMAIN 537 806 PROTEIN KINASE
CC NP_BIND 543 551 ATP (BY SIMILARITY).

FT BINDING 571 571 ATP (BY SIMILARITY).
FT ACT_SITE 675 675 BY SIMILARITY.
FT MOD_RES 515 515 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 701 701 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 705 705 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 706 706 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 816 816 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT SITE 515 515 INTERACTION WITH SHC PROTEIN (BY SIMILARITY).
FT SITE 816 816 INTERACTION WITH PLC-GAMMA-1 (BY SIMILARITY).
FT CARBOHYD 67 67 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 95 95 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 121 121 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 254 254 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 280 280 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 325 325 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 411 411 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPPLIC 466 476 PASVYSNDDDS -> EVLFKIPLDG (IN ISOFORM GP95-TRKB/T1).
FT VARSPPLIC 477 821 MISSING (IN ISOFORM GP95-TRKB/T1).
SQ SEQUENCE 821 AA; 92133 MW; 50E08D5FF6B68F30 CRC64;

Query Match 13.28; Score 648.5; DB 1; Length 821;
Best Local Similarity 30.14; Pred. No. 2.1e-27;
Matches 201; Conservative 72; Mismatches 188; Indels 207; Gaps 23;

QY 373 SPALGTFPPAPAPWPPPPPTNFSSLEPRGQPPVAKAESPPAIIIGCVATIIILL 432
DB 217 SCVSGDPLPLTWVDNLVSKHNETSHGQSLRTNISSDQKIOCV----- 267
QY 433 IIALMLRLHWRLLSKAERVLVEELTVHLV---PGDTLLINRRPGPREPP----- 482
DB 268 -----AENLVGSDQSVNLTVFAFTITL-----ESPISDHHMC 302
QY 483 -PTQEPFRGPNPHSAPCVNGS-----ALLSNPA-----Y 513
DB 303 IPF---TVRGNPKPALOMFYNGALINESKYICTKIHVTNHTYHGCLQIDNPHTMNGDY 359
QY 514 RLL-----ATYARPPRGCGPPTPAKAKTNTQAISGDMEP--E 551
DB 360 TLMAKNEYGDEROISAHFMGRGVDYETNPVPEVLDEWTPPTDI---GDTTKNSNE 415
QY 552 KPGAPLLPPPPONSVPYAEADIVTLQGV-----RS 608
DB 416 IFTSDVADQSNRELSYAAVVYASVGFCLLVALLKLARHSFGMKGPASVINDDD 475
QY 581 -----TGVTVAVPALPGAVGDP--PRVDFP-----RS 608
DB 476 SASPLHHSNGSWTPSSSEGGPDVILGKIPVENPQFGITNSQLKPDTEVOHIKRH 535
QY 609 RLRFKEKLGEGGGEVHLC---VDSQDVLVSDFLPNAVKGHLLVAVYILRPDARKNA 665
DB 536 NIVLKRELGGAGKVFACVNLCPED-----KILVAVATLK--DASDNA 580
QY 666 SFSLSRNDPLKVKIMSRKDPNIIRLGVQVODPLCATITDMENGDNQFASQOLE 725
DB 581 -----RKDFHRAELLTNQHHEHYKVFYCVBGDDLINVEFMKGKGLKFLRAHGPD 634
QY 726 D-KAAGAPGDDGOAAGPT--ISTPMLIHVAQAISAGRYLATINFAHDLATRNCLVGEN 783
DB 635 AVLMAGNP-----PRELTQSOMLHIAQIAAGVYLAISOHFVRDLATRNCLVGEN 686
QY 784 FTIKINDFGMSRLVAGDYRYRQGRAVLPTRMMAMECILMGKTTASDVAFVTLMEVL 843
DB 687 LLYKIDFGMSRKYVISTDIYRGVHTMLPIRMPPEISIMIRKKTSTSDVSLVLIWEIF 746
QY 844 MLCRAQPFQQLDEQVIEANGFEFFRDGROVYLSRPACPOGLYEIMLRCSRESSEORRP 903

DB 747 TYR-CPWOLSNNEVEICT-----TQGR-VLQRPCTQPEVEYELMGCGQRPHPRKN 798
 OY 904 FSQHLNRL 911
 DB 799 IKSITL 806

RESULT 7
 TRKB_RAT STANDARD: PRT: 821 AA.
 ID TRKB_RAT 063604: 063605: 063606:
 AC 063604: 063605: 063606: (Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE BDNF/NT-3 growth factors precursor (EC 2.7.1.112) (TRKB
 tyrosine kinase) (GPI45-TRKB/GP95-TRKB) (TRKB-B).
 GN NTRK2 OR TRKB.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.
 RC TISSUE=Cerebellum;
 RX MEDLINE=91094826; PubMed=1846020;
 RA Middlemas D.S., Lindberg R.A., Hunter T.;
 RT "trkb, a neural receptor protein-tyrosine kinase: evidence for a
 full-length and two truncated receptors";
 RL Mol. Cell. Biol. 11:143-153(1991).
 RN [2]
 RP PHOSPHORYLATION SITES.
 RX MEDLINE=94149017; PubMed=8106527;
 RA Middlemas D.S., Meisenhelder J., Hunter T.;
 RT "Identification of trkb autophosphorylation sites and evidence that
 phosphotyrosine C-gamma 1 is a substrate of the trkb receptor";
 RL J. Biol. Chem. 269:5458-5466(1994).
 CC -1- FUNCTION: RECEPTOR FOR BRAIN-DERIVED NEUROTROPHIC FACTOR (BDNF),
 NEUROTROPHIN-3 AND NEUROTROPHIN-4/5 BUT NOT NERVE GROWTH FACTOR
 (NGF). INVOLVED IN THE DEVELOPMENT AND/OR MAINTENANCE OF THE
 NERVOUS SYSTEM. THIS IS A TYROSINE-PROTEIN KINASE RECEPTOR. KNOWN
 SUBSTRATES FOR THE TRK RECEPTORS ARE SHC, PI-3 KINASE, AND PLC-
 GAMMA-1.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
 tyrosine phosphate.
 CC -1- SUBUNIT: EXISTS IN A DYNAMIC EQUILIBRIUM BETWEEN MONOMERIC (LOW
 AFFINITY) AND DIMERIC (HIGH AFFINITY) STRUCTURES (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: TYPE I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 3 ISOFORMS: GPI45-TRKB (SHOWN
 HERE), T1/GP95-TRKB AND T2: ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: THE DIFFERENT FORMS ARE DIFFERENTIALLY
 EXPRESSED IN VARIOUS CELL TYPES. THE T2 ISOFORM IS PRIMARILY
 EXPRESSED IN NEURONS.
 CC -1- LIGAND-MEDIATED AUTO-PHOSPHORYLATION.
 CC -1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
 PROTEIN KINASES. TRK-TYPE SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
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 CC
 CC EMBL: M55291: AAA42279.1: -
 DR EMBL: M55292: AAA42280.1: -
 DR EMBL: M55293: AAA42281.1: -
 DR HSSP: P11362: IAGW.
 DR InterPro: IPR000719; Euk_Pkinase.
 DR InterPro: IPR003006; Ig_MHC.

DR InterPro: IPR003598; Ig_C2.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR000483; LRR_Cterm.
 DR InterPro: IPR000372; LRR_Nterm.
 DR InterPro: IPR002011; Receptor_Tyr_Kin_II.
 DR InterPro: IPR001245; Tyr_Pkinase.
 DR Pfam: PF00047; Ig_1.
 DR Pfam: PF00560; LRR_1.
 DR Pfam: PF01463; LRRCT_1.
 DR Pfam: PF01462; LRRNT_1.
 DR Pfam: PF00069; Pkinase_1.
 DR PRINTS: PR00109; TYRKINASE.
 DR SMART: SM00408; IGC2_1.
 DR SMART: SM00082; LRCT_1.
 DR SMART: SM00013; LRRNT_1.
 DR SMART: SM00219; TYRK_1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP_1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR_1.
 DR PROSITE: PS00239; RECEPTOR_TYR_KIN_II_1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM_1.
 KW Transferase; Tyrosine-protein kinase; Transmembrane; ATP-binding;
 KW Phosphorylation; Receptor; Glycoprotein; Neurogenesis; Signal;
 KW Leucine-rich repeat; Repeat; Immunoglobulin domain;
 KW Alternative splicing.
 FT SIGNAL 1 31
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 FT MOD_RES 705 705
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 FT VARSPLIC 821 821
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 FT VARSPLIC 475 821
 FT SEQUENCE 821 AA; 92186 MW; 0DDACCA212CDA0E CRC64;

Query Match 13.2%; Score 648.5; DB 1; Length 821;
 Best Local Similarity 30.1%; Pred. No. 2.1e-27;
 Matches 201; Conservativity 72; Mismatches 188; Indels 207; Gaps 23;
 OY 373 SPALGCTPPAPMPPGPPPTFSSLELEPGQGVAAAGSPYALIGCLVAITLLLL 432
 DB 217 SCSVGGLPLTLTYMDVGNLVSKHNNETSHQTGSLRITNISSDDSGKQISCV----- 267

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OY 433 ITALMLRLMRRLSKARRVLEELVYHLSV---PGDTILINRPGPREP----- 482
DB 268 -----XENLVGEDQDSNLYLVHAPRTITFL-----ESPSTDHMC 302
OY 483 -RYGEPRRGNPSPAPCPVNGS-----ALLSNPA-----Y 513
DB 303 IFF---TYRGNKPKALQWNYNCAIINESKYICTKHVTNHTEYHCCLOLDNPTNNGDY 359
OY 514 RLL-----ATYARPPRGPPPTAMAKPTNTQAYSGDYMEP--E 551
DB 360 TLMANEXGKDEROISAHFMGRPGVDYETENPNYREVLYEDMTPTPDI---GDTINKSE 415
OY 552 KRGAPLLPPPPONSYPHYAADIYTLQV----- 580
DB 416 IPSTVDADQTNKEHLSYAVAVVYASVGFCLVMLLLKLARSKFKGKSPASVISND 475
OY 581 -----TGNTYAVVAPALPPGAVDGP--PRYDFP-----RS 608
DB 476 SASPLHISNGSNTPSSSEGGPDVAITGMTKIPVTEENPOYEGITNSQLKPDFTVOHIRH 535
OY 609 RLRREKLGEQGFGEVHLCE--VDSPODLVSLDFPLNVRKGHPLVAVKILRPDATRNA 665
DB 536 NYLKRRELGEGAFKVFIAECYNLCPEOD-----KLVAVKTLK-DASDA 580
OY 666 SFSLESRNDFLKEVKYIMRLDPNITRILGYCVODDPLCMITDIWENGDLNOFLSAHOLE 725
DB 581 -----RQDFHREBELNLQHEHIVKRYGVCEDDPLIMVEFYKHKHDLNKLFLAHPGD 634
OY 726 D-KAEGAPGQGAQGP--ISYPMILHVAQAQIASGMBRYLATLNVRHDLATRNQLVEN 783
DB 635 AVLAHEGMP-----PTELTOSQMLHQAQIAGVYLAHQHVAHDLATRNQLVEN 686
OY 784 FTIKIADGSMRLYAGDYRYRQGRAPVLPIRMAMECIIMKFTYASDVMAFGVTLMEVL 843
DB 687 LLVKIGRSGMRDYSYDYRYVGGHTMLPIRMMPRESIMYKFTTESVMSGLVYLWEIF 746
OY 844 MLCRAQPPGQULTDEQVYNAGEFFPRDQROYLLSPRACPOGLYELMLRCSRESEQRP 903
DB 747 TYGK-RQPYQLSNNEVICI-----TQGR--VLQRPFTCPQEVYELMGCWQREPHTRKN 798
OY 904 FSOLHRL 911
DB 799 IKNHTLL 806

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RT "Expression and binding characteristics of the BDNF receptor chick
trkb."
RL Development 119:545-558(1993).
CC -1- FUNCTION: RECEPTOR FOR BRAIN-DERIVED NEUROTROPHIC FACTOR (BDNF),
CC NEUROTROPHIN-3 AND NEUROTROPHIN-4/5 BUT NOT NERVE GROWTH FACTOR
CC (NGF). INVOLVED IN THE DEVELOPMENT AND/OR MAINTENANCE OF THE
CC NERVOUS SYSTEM. THIS IS A TYROSINE-PROTEIN KINASE RECEPTOR. KNOWN
CC SUBSTRATES FOR THE TRK RECEPTORS ARE SHC, PI-3 KINASE, AND PLC-
CC GAMMA-1 (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
CC tyrosine phosphate.
CC -1- SUBUNIT: EXISTS IN A DYNAMIC EQUILIBRIUM BETWEEN MONOMERIC (LOW
CC AFFINITY) AND DIMERIC (HIGH AFFINITY) STRUCTURES (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: A TRUNCATED NON-CATALYTIC FORM WHICH
CC FUNCTION REMAINS STILL UNCLEAR IS PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -1- PTM: LIGAND-MEDIATED AUTO-PHOSPHORYLATION.
CC -1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES. TRK-TYPE SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 2 LEUCINE-RICH REPEATS (LRR).
CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC
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CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: X77251; CA54468.1; -
CC EMBL: X77252; CA54469.1; -
CC EMBL: X74109; CA52210.1; -
CC HSPSP; P11362; IFC1.
CC InterPro: IPR000719; Euk_Pkinase.
CC InterPro: IPR003006; Ig_MHC.
CC InterPro: IPR003598; Ig_C2.
CC InterPro: IPR001611; LRR.
CC InterPro: IPR000483; LRR_Cterm.
CC InterPro: IPR000372; LRR_Nterm.
CC InterPro: IPR002011; Receptor_ty_r_kin_II.
CC InterPro: IPR001245; Tyr_Pkinase.
CC Pfam: PF00047; Ig_1.
CC Pfam: PF00560; LRR_1.
CC Pfam: PF00463; LRRCT_1.
CC Pfam: PF00069; Pkinase_1.
CC PRINTS: PR00109; TYRKINASE.
CC SMART: SM00408; IGC2_1.
CC SMART: SM00082; LRRCT_1.
CC SMART: SM00013; LRRNT_1.
CC SMART: SM00219; TYRK1_1.
CC PROSITE: PS00107; PROTEIN_KINASE_ATP_1.
CC PROSITE: PS00109; PROTEIN_KINASE_TYR_1.
CC PROSITE: PS50011; PROTEIN_KINASE_DOM_1.
CC PROSITE: PS00239; RECEPTOR_TYR_KIN_II_1.
CC Transferrase: Tyrosine-protein kinase; Transmembrane; ATP-binding;
CC Phosphorylation; Receptor; Glycoprotein; Neurogenesis; Signal;
CC Leucine-rich repeat; Repeat; Alternative splicing;
CC Immunoglobulin domain.
CC SIGNAL 1 31
CC CHAIN 32 818
CC DOMAIN 32 426
CC TRANSEM 427 450
CC REPEAT 451 818
CC REPEAT 95 92
CC DOMAIN 213 269
CC DOMAIN 300 364
CC DOMAIN 534 803
CC NF_BIND 540 548
CC BINDING 568 568
CC ACT_SITE 672 672

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RA MEDLINE-94116452; Pubmed-8287802; Kolbeck R., Pottgiesser J.,
RA Dechant G., Biffo S., Okazawa H.,
RA Barde Y.A.;

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FT MOD_RES 512 512 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 698 698 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 702 702 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 703 703 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 813 813 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT SITE 512 512 INTERACTION WITH SHC PROTEIN (BY SIMILARITY).
FT SITE 813 813 INTERACTION WITH PLC-GAMMA-1 (BY SIMILARITY).
FT CARBOHYD 66 66 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 94 94 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 120 120 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 199 199 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 204 204 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 226 226 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 233 233 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 287 287 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 324 324 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 337 337 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 408 408 N-LINKED (GLCNAC...) (POTENTIAL).
FT VARSPIC 462 520 GRSVTSNDSDASPLHHSNGSNTSSSGGPDVYIGMT KIPVLENPQYFGISPLNSQL -> VHGKVGGLVDQIMLSIQ DCDNEQVATVNSDVHNSSTASDNRRGLGFVLFKIPLDG (IN TRUNCATED ISOFORM).
FT VARSPIC 521 818 MISSING (IN TRUNCATED ISOFORM).
SQ SEQUENCE 818 AA, 91736 MW, D1BA39E2092B2152 CRC64;

Query Match 13.1%; Score 648; DB 1; Length 818;
Best Local Similarity 34.2%; Pred. No. 2.3e-27;
Matches 176; Conservative 71; Mismatches 149; Indels 118; Gaps 19;

OY 446 LLSKARRVLEELTYH-LSVPDQTLINRRPREPPPOE---PRPGNPPH----- 495
DB 360 LLAKNYGEDEKRVDAHFMSVDPD-----GSGPIVDPDVEYETTPNDGDTNNSNQI 413
OY 496 SARCVENG-----SALLSNPARYLLATVARRP---RGSGPTPAAPAKR 537
DB 414 TSDVSNKKEHEDSIYVVYVIGIALVCTGIVMLILKFRHSKFGKGP----- 463
OY 538 TMTQAVSGDYMEKEKGPAPLPAPPONSYPHYAEDIVTLOGVTGNTYAVPALPGAVG 597
DB 464 --SSVISND--DSDASPL-----HHISNGSNTPSSSEGGPDVYIGMTKIPVI 507
OY 598 DDPFRPDRSRRLR-----FKKIEGEGFGEVHICE---VDSPODLSLDF 640
DB 508 ENPQYFGITNSOLKPDPTFVOHIKRNIYVKRELGEAGFVFLAECYNLCPEOD----- 561
OY 641 PLNVKRGHPLLVAKILRPDATKNASFSLFSRNDPLKEYVIRLDPNITIRLLGVYOD 700
DB 562 -----KILVAVKTLK-DASDNA-----KDFHEAELLTNLOHEHVKYGVCEVG 606
OY 701 DPLCMITDYMENDLNQPLSAHOLEDKAEGAPDGOAAG---PTISYMLLHVAAQIA 757
DB 607 DPLIMFEYMKHGDNLKFLRAH-----GPDVAVLMEGNRPALDTQGMHIAQIA 657
OY 758 SGMRVYATLNFVARDLATRNCLVGENFTIKIADFGSRNLIADGYRVQGRAVLPIRMA 817
DB 658 ACRYVLAASHFVARDLATRNCLVGENMLVKGIFGMSRDVYSTDYRYVSGHTMLPIRMP 717
OY 818 WECILMGKFTTASDVAFVLTLMVLMCRAOPGTLDEOVLENMGEFFRDGROVYLS 877
DB 718 PPSIMKRKTTSDVMSLVLVEITTYGR-QPWYLSNNEVEICT-----TQGR---VLO 769
OY 878 RPPACPGQLEMLRCMSRESEQRPFSQLHREL 911
DB 770 RPTCPKEYYDMLGCMQREPRHRLNIKEIHSLL 803

RESULT 9
TRKB_HUMAN STANDARD; PRT; 822 AA.
AC Q16620; Q16675;

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DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE BDNF/NT-3 growth factors receptor precursor (EC 2.7.1.112) (TRKB
DE tyrosine kinase) (GP145-TRKB) (TRK-B).
GN NTRK2 OR TRKB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_Taxid=9606;
OX [1]
PP SEQUENCE FROM N.A. (LONG FORM).
PP TISSUE-Hippocampus;
RC MEDLINE=95109922; PubMed=7789988;
RA Nakagawara A., Liu X.-G., Ikegaki N., White P.S., Yamashiro D.J.,
RA Nycum L.M., Biegel J.A., Brodeur G.M.;
RT "Cloning and chromosomal localization of the human TRK-B tyrosine
RT kinase receptor gene (NTRK2).";
RL Genomics 25:538-546(1995).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE (LONG AND TRUNCATED FORMS).
RP TISSUE-Brain;
RC MEDLINE=95123473; PubMed=7823156;
RA Shelton D.L., Sutherland J., Gripp J., Camerito T., Armanini M.P.,
RA Phillips H.S., Carroll K., Spencer S.D., Levinson A.D.;
RT "Human trks: molecular cloning, tissue distribution, and expression
RT of extracellular domain immunoadhesins.";
RL J. Neurosci. 15:477-491(1995).
RN [3]
RP SEQUENCE FROM N.A. (TRUNCATED FORMS).
RP TISSUE-Hippocampus;
RC MEDLINE=95022162; PubMed=7936202;
RA Allen S.J., Dawbarn D., Eckford S.D., Wilcock G.K., Ashcroft M.,
RA Colebrook S.M., Feeney R., Macgowan S.H.;
RT "Cloning of a non-catalytic form of human trkb and distribution of
RT messenger RNA for trkb in human brain.";
RL Neuroscience 60:825-834(1994).
RN [4]
RP FUNCTION: RECEPTOR FOR BRAIN-DERIVED NEUROTROPHIC FACTOR (BDNF),
RP NEUROTROPHIN-3 AND NEUROTROPHIN-4/5 BUT NOT NERVE GROWTH FACTOR
RP (NGF). INVOLVED IN THE DEVELOPMENT AND/OR MAINTENANCE OF THE
RP NERVOUS SYSTEM. THIS IS A TYROSINE-PROTEIN KINASE RECEPTOR. KNOWN
RP SUBSTRATES FOR THE TRK RECEPTORS ARE SHC, PI-3 KINASE, AND PLC-
RP GAMMA-1.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
CC tyrosine phosphate.
CC -1- SUBUNIT: EXISTS IN A DYNAMIC EQUILIBRIUM BETWEEN MONOMERIC (LOW
CC AFFINITY) AND DIMERIC (HIGH AFFINITY) STRUCTURES (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: TYPE I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: A TRUNCATED NON-CATALYTIC FORM WHICH
CC FUNCTION REMAINS STILL UNCLEAR IS PRODUCED BY ALTERNATIVE
CC SPLICING. THE RATIO OF FULL-LENGTH TO TRUNCATED FORM IS HIGHER IN
CC FETAL THAN IN ADULT BRAIN.
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED, MAINLY IN THE NERVOUS
CC TISSUE. IN THE CNS, EXPRESSION IS OBSERVED IN THE CEREBRAL CORTEX,
CC HIPPOCAMPUS, THALAMUS, CHOROID PLEXUS, GRANULAR LAYER OF THE
CC CEREBELLUM, BRAIN STEM, AND SPINAL CORD. IN THE PERIPHERAL NERVOUS
CC SYSTEM, IT IS EXPRESSED IN MANY CRANIAL GANGLIA, THE OPHTHALMIC
CC NERVE, THE VESTIBULAR SYSTEM, MULTIPLE FACIAL STRUCTURES, THE
CC SUBMAXILLARY GLANDS, AND DORSAL ROOT GANGLIA.
CC -1- PTM: LIGAND-MEDIATED AUTO-PHOSPHORYLATION.
CC -1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES. TRK-TYPE SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 2 LEUCINE-RICH REPEATS (LRR).
CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC
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DR EMBL: U12140; AAC5371.1; -
 DR EMBL: S76473; AAB33109.1; -
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 DR EMBL: X75958; CAAS3571.1; -
 DR HSSP: P11362; IAGW.
 DR MIM: 600456; -
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003598; Ig_c2.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR000483; LRR_cterm.
 DR InterPro: IPR000372; LRR_Nterm.
 DR InterPro: IPR002011; Receptor_Tyr_Kin_II.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00047; Ig_1.
 DR Pfam: PF00560; LRR_1.
 DR Pfam: PF01463; LRRCT_1.
 DR Pfam: PF01462; LRRNT_1.
 DR Pfam: PF00069; pkinase_1.
 DR PRINTS: PR00109; TYRKINASE.
 DR SMART: SM00408; IGC2_1.
 DR SMART: SM00082; LRRCT_1.
 DR SMART: SM00013; LRRNT_1.
 DR SMART: SM00219; TYKC_1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP_1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR_1.
 DR PROSITE: PS00239; RECEPTOR_TYR_KIN_II_1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM_1.
 DR Transferase: Tyrosine-protein kinase; Transmembrane; ATP-binding;
 KW Phosphorylation; Receptor; Glycoprotein; Neurogenesis; Signal;
 KW Leucine-rich repeat; Repeat; Immunoglobulin domain;
 KW Alternative splicing; Polymorphism.
 FT CHAIN 1 31
 FT DOMAIN 32 430
 FT TRANSMEM 431 454
 FT DOMAIN 455 822
 FT REPEAT 72 93
 FT REPEAT 96 117
 FT DOMAIN 214 270
 FT DOMAIN 301 365
 FT DOMAIN 338 807
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 FT CARBOHYD 338 338
 FT CARBOHYD 412 412
 FT CARBOHYD 467 477
 FT VARSPPLIC 478 822
 FT VARIANT 338 338
 FT SEQUENCE 822 AA; 91998 MW; 2FEB915948FDD13 CRC64;

Query Match 13.1%; Score 645; DB 1; Length 822;
 Best Local Similarity 46.5%; Pred. No. 3,3e-27;
 Matches 144; Conservative 45; Mismatches 79; Indels 42; Gaps 10;
 QY 607 RSRTRKEKLGEGQFGEVNLCE---VDSPODLVSLDFPLNVRKGHLYVAVITLRDARK 663
 DB 535 RSNIVAKRELKGEAGFKVFLAEVCYNLCPEOD-----KILVAVTLK-DASD 579
 QY 664 NASFSLFSRNDLFKEVKISRLKDPNIIRLIGCVQVODDFLCMTDMNGDNLQFSLAQ 723
 DB 580 NA-----KDDPRRELELTNLQHEHIVAFYGVGVGDELINFEFMKGDGLNFKFRAAG 633
 QY 724 LED-KAEGAPGDGAQAQPT-ISYPMLLHVAQAISGKRYATLNFVRDLATRNCLVG 781
 DB 634 PDAVLAEGNP-----PTELQSQMHLIAQIAAGVYLLASQFVHRDLATRNCLVG 685
 QY 782 ENFTIKIADFGMSRLNIYADYRVQGRAVLPFRMAAMECILMGKFTTASDVAFCYTLNE 841
 DB 686 ENLVKIGDFGMSRDVYSTDYRVGHTMLPIRMMPESIMYRKFTTESDVSIGVLMVE 745
 QY 842 VLMLCRAOPFGQITDQVFNENNGEFPFRDQROVYLSRPPACPGYLEMLRCMSRESER 901
 DB 746 IFTYGR-QPMYQLSNNEVEICT-----TQGR-VLQRPRTCPQEVYELMLGCMQRPBMR 797
 QY 902 PFSQLRFL 911
 DB 798 KNKGHTL 807

RESULT 10
 ID TRKA_HUMAN STANDARD; PRT; 796 AA.
 AC P04629; P08119; Q9U107;
 DT 13-AUG-1987 (Rel. 05; Created)
 DT 15-JUL-1998 (Rel. 36; Last sequence update)
 DT 16-OCT-2001 (Rel. 40; Last annotation update)
 DE High affinity nerve growth factor receptor precursor (EC 2.7.1.112)
 DE (TRK1 transforming tyrosine kinase protein) (p140-TrkA) (Trk-A).
 GN NTRK1 OR TRK.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (TRKA-I ISOFORM).
 RC TISSUE=colon.
 RX MEDLINE=89181575; PubMed=2927393;
 RA Martin-Zanca D., Oskam R., Mitra G., Copeland T.D., Barbacid M.;
 RT "Molecular and biochemical characterization of the human trk proto-oncogene";
 RL Mol. Cell. Biol. 9:24-33(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=95123473; PubMed=7823156;
 RA Shelton D.L., Sutherland J., Gripp J., Camerato T., Armanini M.P.,
 RA Phillips H.S., Carroll K., Spencer S.D., Levinson A.D.;
 RT "Human trks: molecular cloning, tissue distribution, and expression of extracellular domain immunoadhesins";
 RL J. Neurosci. 15:477-491(1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97435581; PubMed=9290260;
 RA Indo Y., Mardy S., Tsunuma M., Katim M.A., Matsuda I.;
 RT "Structure and organization of the human trkA gene encoding a high affinity receptor for nerve growth factor";
 RL Jpn. J. Hum. Genet. 42:343-351(1997).
 RN [4]
 RP SEQUENCE OF 399-796 FROM N.A.
 RX MEDLINE=86146854; PubMed=2869410;
 RA Martin-Zanca D., Hughes S.H., Barbacid M.;
 RT "A human oncogene formed by the fusion of truncated tropomyosin and protein tyrosine kinase sequences.";

RL Nature 319:743-748(1986).
RN [5]
RP SEQUENCE OF 399-796 FROM N.A.
RX MEDLINE-88196074; PubMed-2966065;
RA Kozma S.C., Redmond S.M.S., Saurer S.M., Groner B., Hynes N.E.;
RT "Activation of the receptor kinase domain of the trk oncogene by
RT recombination with two different cellular sequences.";
RL EMO J. 7:147-154(1988).
RN [6]
RP FUNCTION.
RX MEDLINE-91218846; PubMed-1850821;
RA Hemstead B.L., Martin-Ganca D., Kaplan D.R., Parada L.F., Chao M.V.;
RT "High-affinity NGF binding requires coexpression of the trk proto-
RT oncogene and the low-affinity NGF receptor.";
RL Nature 350:678-683(1991).
RN [7]
RP FUNCTION.
RX MEDLINE-91191557; PubMed-1849459;
RA Klein R., Jing S., Nanduri V., O'Rourke E., Barbacid M.;
RT "The trk proto-oncogene encodes a receptor for nerve growth factor.";
RL Cell 65:189-197(1991).
RN [8]
RP ALTERNATIVE SPLICING.
RX MEDLINE-93315496; PubMed-8325889;
RA Barker P.A., Lomen-Hoeft C., Gensch E.M., Meakin S.O., Glass D.J.,
RT Shooter E.M.;
RT "Tissue-specific alternative splicing generates two isoforms of the
RT trkA receptor.";
RL J. Biol. Chem. 268:15150-15157(1993).
RN [9]
RP MUTAGENESIS OF TYR-791.
RX MEDLINE-94179299; PubMed-7510697;
RA Loeb D.M., Stephens R.M., Copeland T.D., Kaplan D.R., Greene L.A.;
RT "A trk nerve growth factor (NGF) receptor point mutation affecting
RT interaction with phospholipase C-gamma 1 abolishes NGF-promoted
RT peripheral induction but not neurite outgrowth.";
RL J. Biol. Chem. 269:8901-8910(1994).
RN [10]
RP MUTAGENESIS, AND PHOSPHORYLATION SITES.
RX MEDLINE-94206546; PubMed-8155326;
RA Stephens R.M., Loeb D.M., Copeland T.D., Pawson T., Greene L.A.,
RT Kaplan D.R.;
RT "Trk receptors use redundant signal transduction pathways involving
RT SHC and PLC-gamma 1 to mediate NGF responses.";
RL Neuron 12:691-705(1994).
RN [11]
RP STRUCTURE BY NMR OF 489-500.
RX MEDLINE-96097066; PubMed-8524391;
RA Zhou M.M., Ravichandran K.S., Olejniczak E.F., Petros A.M.,
RA Meadows R.P., Sattler M., Hailan J.E., Wade W.S., Burakoff S.J.,
RA Feak S.W.;
RT "Structure and ligand recognition of the phosphorylase binding
RT domain of Shc.";
RL Nature 378:584-592(1995).
RN [12]
RP VARIANT CIPA ARG-577.
RX MEDLINE-96331294; PubMed-8696348;
RA Indo Y., Tsutsumi M., Hayashida Y., Karim M.A., Ohta K., Kawano T.,
RA Mitsubuchi H., Tonoki H., Aways Y., Matsuda I.;
RT "Mutations in the TRKA/NGF receptor gene in patients with congenital
RT insensitivity to pain with anhidrosis.";
RL Nat. Genet. 13:485-488(1996).
RN [13]
RP VARIANT CIPA PRO-780.
RX MEDLINE-99192367; PubMed-10090906;
RA Greco A., Villa R., Tupino B., Romano L., Penso D., Pierotti M.A.;
RT "A Novel NTRK1 Mutation Associated with Congenital Insensitivity to
RT Pain with Anhidrosis.";
RL Am. J. Hum. Genet. 64:1207-1210(1999).
RN [14]
RP VARIANTS CIPA P-213; W-649 AND S-714, AND VARIANTS S-85; Y-604 AND
RP V-613.
RX MEDLINE-99264238; PubMed-10330344;

RA Mardy S., Miura Y., Endo F., Matsuda I., Sztrika L., Frossard P.,
RA Moosa A., Ismail E.A.R., Macaya A., Andria G., Toscano E., Gibson W.,
RA Graham G.E., Indo Y.;
RT "Congenital insensitivity to pain with anhidrosis: novel mutations in
RT the TRKA (NTRK1) gene encoding a high-affinity receptor for nerve
RT growth factor.";
RL Am. J. Hum. Genet. 64:1570-1579(1999).
RN [15]
RP VARIANTS TYR-604; VAL-613 AND GLN-780.
RX MEDLINE-99371280; PubMed-10443680;
RA Gimm O., Greco A., Hoang-Vu C., Dralle H., Pierotti M.A., Eng C.;
RT "Mutation analysis reveals novel sequence variants in NTRK1 in
RT sporadic human medullary thyroid carcinoma.";
RL J. Clin. Endocrinol. Metab. 84:2784-2787(1999).
RN [16]
RP VARIANT CIPA VAL-587.
RX MEDLINE-99250414; PubMed-10233776;
RA Yotsumoto S., Setoyama M., Hozumi H., Mizoguchi S., Fukumaru S.,
RA Kobayashi K., Saheki T., Kanazaki T.;
RT "A novel point mutation affecting the tyrosine kinase domain of the
RT TRKA gene in a family with congenital insensitivity to pain with
RT anhidrosis.";
RL J. Invest. Dermatol. 112:810-814(1999).
RN [17]
RP VARIANT CIPA LEU-695, AND VARIANT VAL-613.
RX TISSUE-Peripheral blood;
RX MEDLINE-20321341; PubMed-10861667;
RA Shatzky S., Moses S., Levy J., Plinsk V., Hershkovitz E., Herzog L.,
RA Shorer Z., Luder A., Patvardi R.;
RT "Congenital insensitivity to pain with anhidrosis (CIPA) in
RT Israeli-Bedouins: genetic heterogeneity, novel mutations in the
RT TRKA/NGF receptor gene, clinical findings, and results of nerve
RT conduction studies.";
RL Am. J. Med. Genet. 92:353-360(2000).
RN [18]
RP VARIANTS CIPA PRO-93; ARG-522; ARG-577; CYS-654 AND TYR-674.
RX MEDLINE-20435070; PubMed-10982191;
RA Miura Y., Mardy S., Aways Y., Nibel K., Endo F., Matsuda I., Indo Y.;
RT "Mutation and polymorphism analysis of the TRKA (NTRK1) gene encoding
RT a high-affinity receptor for nerve growth factor in congenital
RT insensitivity to pain with anhidrosis (CIPA) families.";
RL Hum. Genet. 106:116-124(2000).
RN [19]
RP VARIANT CIPA ARG-577.
RX MEDLINE-20036616; PubMed-10567924;
RA Greco A., Villa R., Fusetti L., Orlandi R., Pierotti M.A.;
RT "The Gly571Arg mutation, associated with the autonomic and sensory
RT disorder congenital insensitivity to pain with anhidrosis, causes the
RT inactivation of the NTRK1/nerve growth factor receptor.";
RL J. Cell. Physiol. 182:127-133(2000).
CC -1- FUNCTION: REQUIRED FOR HIGH-AFFINITY BINDING TO NERVE GROWTH
CC FACTOR (NGF), NEUROPOPHIN-3 AND NEUROPOPHIN-4/5 BUT NOT BRAIN-
CC DERIVED NEUROTROPHIC FACTOR (BDNF). KNOWN SUBSTRATES FOR THE TRK
CC RECEPTORS ARE SHC, PI-3 KINASE, AND PLC-GAMMA-1. HAS A CRUCIAL
CC ROLE IN THE DEVELOPMENT AND FUNCTION OF THE NOCICEPTIVE RECEPTION
CC SYSTEM AS WELL AS ESTABLISHMENT OF THERMAL REGULATION VIA
CC SWEATING. ACTIVATES ERK1 BY EITHER SHC- OR PLC-GAMMA-1-DEPENDENT
CC SIGNALING PATHWAY.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
CC tyrosine phosphate.
CC -1- SUBUNIT: EXISTS IN A DYNAMIC EQUILIBRIUM BETWEEN MONOMERIC (LOW
CC AFFINITY) AND DIMERIC (HIGH AFFINITY) STRUCTURES.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS, TRKA-I AND TRKA-II (SHOWN
CC HERE). ARE PRODUCED BY ALTERNATIVE SPLICING. BOTH ISOFORMS HAVE
CC SIMILAR BIOLOGICAL PROPERTIES.
CC -1- TISSUE SPECIFICITY: TRKA-II IS PRIMARILY EXPRESSED IN NEURONAL
CC CELLS; TRKA-I IS FOUND IN NON-NEURONAL TISSUES.
CC -1- PTM: LIGAND-MEDIATED AUTO-PHOSPHORYLATION.
CC -1- DISEASE: THE AMINO END OF SEVERAL DIFFERENT CELLULAR PROTEINS
CC (SUCH AS NON-MUSCLE TROPOMYOSIN TM30NM) HAS BEEN FOUND FUSED WITH
CC THE PROTEIN TYROSINE KINASE DOMAIN ENCODED BY NTRK1. THESE SOMATIC
CC REARRANGEMENT CREATES AN ONCOGENIC PROTEIN.

CC -1- DISEASE: DEFECTS IN NTRK1 ARE A CAUSE OF A DISEASE CALLED CIPA;
 CC WHICH IS CHARACTERIZED BY A CONGENITAL INSENSITIVITY TO PAIN,
 CC ANHIDROSIS (ABSENCE OF SWEATING), ABSENCE OF REACTION TO NOXIOUS
 CC STIMULI, SELF-MUTILATING BEHAVIOR, AND MENTAL RETARDATION. THIS
 CC RARE AUTOSOMAL RECESSIVE DISORDER IS ALSO KNOWN AS CONGENITAL
 CC SENSORY NEUROPATHY WITH ANHIDROSIS OR HEREDITARY SENSORY AND
 CC AUTONOMIC NEUROPATHY TYPE IV OR FAMILIAL DYSAUTONOMIA TYPE II.
 CC -1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
 CC PROTEIN KINASES. TRK-TYPE SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 2 LEUCINE-RICH REPEATS (LRR).
 CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC

Query Match 13.0%; Score 642; DB 1; length 796;
 Best Local Similarity 28.6%; Pred. No. 4,5e-27;
 Matches 230; Conservative 87; Mismatches 245; Indels 242; Gaps 32;

QY 238 LDFRKSQELR---VMPGDDYVGSNHSFSGYVEKEFEFRLR-----AFQAM 283
 DB 84 LRLRLGELRLNLTIVKSGRLFAVAPDAFHTPLRLNLSFNALSLSMKTVQGLSLQEL 143
 QY 284 OVHONNMHTLGARLPGVEGRFRGRPAMAGE-----PMRNLGSGNLG 327
 DB 144 VLGNPFLH-----CSCALRM--LQWKEGGLGVPEOKLQCHGQGLAHNPASCG 192
 QY 328 DPRARA---VSVPLGGRVAFRLQC---RFLFAGPWLLESEISFISDVNNSSPALGT 379
 DB 193 VPLTKGVNPASVYGDV---LLRCQVEGRGLQAGWIL----- 229
 QY 380 FPPAPMPPEPPPPNSSLLEPRGQOPVAKAGSPFALLIGLVALILLILLITALLMLM 439
 DB 230 -----TELEQ--SATVAKSGGLPS-----LGLTLAVNTS 256
 QY 440 RLHWRLLSKAERYLEELTLHLSV--PGDTLL-----INNRGPR--- 479
 DB 257 DLNKKNLTCMAENDGCAEAEVQVNVSTFASVQHLTAVENHNCIPRSVVGQAPSLRWL 316
 QY 480 -----EPPPYOEP---PRGNPRSHAPCVNGS--ALLLSNP---AYR 514
 DB 317 FNGSVLNETSFITFELFEPANETVRHGLRLNQPTH---VNNGNNTLLAANPFGASA 372
 QY 515 LLATATYRPP--RGPFRPTAMAKPTNTQAYSQDYNL--PEKP----- 553
 DB 373 SIMAAFNDPEENPEPDPVSEFSPVDNTSGDPVEKKEDETFGVSAVAGLAVFACFL 432
 QY 554 -----GAPLLRPPQNSVPHYAADIYVLQVGTGNTYAVPALRP 593
 DB 433 STILLVLNKCGRNKKGINRPAYLAPEDGLAMSLHF---MTLGGSSLSPTGKSGSLQ 487
 QY 594 GAVGDGPPRVD-----FPRSRLRFKEKLGEGQFGEVHLCEVDS---PODLVSLDFPLNV 644
 DB 488 GHITENQVYSDACVNHKIKRODIVLAKWELEGCAFVFLAECHNLBPDQ----- 537
 QY 645 RKCHPLLVAVKILRPDAKNAFSLFSRNDELKVKIMSKLPDNTIRLIGVCVQDDPLC 704
 DB 538 -----KMLVVK-----ALKKASES--ARQDFQREAEELTLMLOHQHLYRFGVTEGSRPL 586
 QY 705 MTDVYENGDLNQLFSLAHQLEDKAKAGAPGDGAAGPITISYPMILHVAQAISGKRYLA 784
 DB 587 MVEYHNRHGDLPFLSHSGDAKLAGE---DYAPGP--LGIGQLLAVASQVAGWYLA 642
 QY 765 TLNFVHRLDTRNCLVGENFTIKIADFGMSRLYAGDYRVQGRAVLPFRMAECLILMG 824
 DB 643 GLHFVHRDLATRNCLVGGGLVYIGDFGMSRDISTDYRVGGRMLPIFRMPPELILVR 702
 QY 825 KFTTASDVAFVCTTLEVYMLCAQPPFGOLTDQVLENAGGEPRDQGRQVYLSRPACQ 884
 DB 703 KFTTEDVMSFGVLTWEIIFYGK--QPMYOLISNTEAIDCI-----TOGRE--LERPRACP 754
 QY 885 GLYELMLRCMSRESEORPPSOLH 908
 DB 755 EYVAIMRGCMQRPQDRHSIKDVH 778

RESULT 11

TRKA_RAT	STANDARD;	PRT;	799 AA.
ID	TRKA_RAT		
AC	P53739;		
DT	01-JUN-1994 (Rel. 29, Created)		
DT	01-JUN-1994 (Rel. 29, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	High affinity nerve growth factor receptor precursor (EC 2.7.1.112)		
DE	(p140-TRKA) (Slow nerve growth factor receptor) (Trk-A).		
GN	NRK1 OR TRKA OR TRK.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NBLTaxid-10116;		
RN	[1]		
RP	SEQUENCE FROM N.A. (TRKA-II ISOFORM).		
RX	MEDLINE-92196121; PubMed-1312719;		
RA	Meakin S.O., Suter U., Drinkwater C.C., Welcher A.A., Shooter E.M.,		
RT	"The rat trk protooncogene product exhibits properties characteristic		
RT	of the slow nerve growth factor receptor.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 89:2374-2378(1992).		
RN	[2]		
RP	ALTERNATIVE SPLICING.		
RX	MEDLINE-93315496; PubMed-8325889;		
RA	Barker P.A., Lomen-Hoerth C., Gensch E.M., Meakin S.O., Glass D.J.,		
RT	Shooter E.M.,		
RT	"Tissue-specific alternative splicing generates two isoforms of the		
RL	trkA receptor.";		
RL	J. Biol. Chem. 268:15150-15157(1993).		
CC	-1- FUNCTION: REQUIRED FOR HIGH-AFFINITY BINDING TO NERVE GROWTH		
CC	FACTOR (NGF), NEUROTROPHIN-3 AND NEUROTROPHIN-4/5 BUT NOT BRAIN-		
CC	DERIVED NEUROTROPHIC FACTOR (BDNF). KNOWN SUBSTRATES FOR THE TRK		
CC	RECEPTORS ARE SHC, PI-3 KINASE, AND PLC-GAMMA-1. HAS A CRUCIAL		
CC	ROLE IN THE DEVELOPMENT AND FUNCTION OF THE NOCICEPTIVE RECEPTION		
CC	SYSTEM AS WELL AS ESTABLISHMENT OF THERMAL REGULATION VIA		
CC	SWEATING. ACTIVATES ERK1 BY EITHER SHC- OR PLC-GAMMA-1-DEPENDENT		
CC	SIGNALING PATHWAY (BY SIMILARITY).		
CC	-1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein		
CC	tyrosine phosphate.		
CC	-1- SUBUNIT: EXISTS IN A DYNAMIC EQUILIBRIUM BETWEEN MONOMERIC (LOW		
CC	AFFINITY) AND DIMERIC (HIGH AFFINITY) STRUCTURES.		
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.		
CC	-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: TRKA-I AND TRKA-II (SHOWN		
CC	HERE); ARE PRODUCED BY ALTERNATIVE SPLICING. BOTH ISOFORMS HAVE		
CC	SIMILAR BIOLOGICAL PROPERTIES.		
CC	-1- TISSUE SPECIFICITY: TRKA-II IS PRIMARILY EXPRESSED IN NEURONAL		
CC	CELLS; TRKA-I IS FOUND IN NON-NEURONAL TISSUES.		
CC	-1- PTM: LIGAND-MEDIATED AUTO-PHOSPHORYLATION.		
CC	-1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-		
CC	PROTEIN KINASES. TRK-TYPE SUBFAMILY.		
CC	-1- SIMILARITY: CONTAINS 2 LEUCINE-RICH REPEATS (LRR).		
CC	-1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.		
CC	-1- This SWISS-PROT entry is copyright. It is produced through a collaboration		
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation		
CC	at the European Bioinformatics Institute. There are no restrictions on its		
CC	use by non-profit institutions as long as its content is in no way		
CC	modified and this statement is not removed. Usage by and for commercial		
CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/		
CC	or send an email to license@sib-sib.ch).		
CC	EMBL: M85214; AAA2286.1; -		
DR	EMBL: L12225; -; NOT_ANNOTATED_CDS.		
DR	PIR: A41981; TVRTB.		
DR	HSSP: P11362; IFGR.		
DR	InterPro: IPR000719; Euk_pkinase.		
DR	InterPro: IPR003599; IG.		
DR	InterPro: IPR001611; LRR.		
DR	InterPro: IPR000483; LRR_Cterm.		
DR	InterPro: IPR002011; Receptor_Tyr_kin_II.		
DR	InterPro: IPR001245; Tyr_pkinase.		
DR	Pfam: PF00560; LRR; 2.		

DR Pfam; PF00069; kinase; 1.
 DR PRINTS; PRO0109; TYRKINASE.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00082; LRCT; 1.
 DR SMART; SM00219; TYRC; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
 DR Transferase; Tyrosine-protein kinase; ATP-binding; phosphorylation;
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
 KW Leucine-rich repeat; Immunoglobulin domain; Neurogenesis;
 KW Alternative splicing.
 FT CHAIN 1 32
 FT SIGNAL 1 32
 FT CHAIN 33 799
 FT DOMAIN 33 418
 FT TRANSMEM 419 442
 FT DOMAIN 443 799
 FT REPEAT 90 113
 FT REPEAT 114 137
 FT DOMAIN 213 271
 FT DOMAIN 301 368
 FT NP_BIND 519 527
 FT BINDING 547 547
 FT ACT_SITE 653 653
 FT MOD_RES 499 499
 FT MOD_RES 679 679
 FT MOD_RES 683 683
 FT MOD_RES 684 684
 FT MOD_RES 794 794
 FT SITE 499 499
 FT SITE 794 794
 FT SITE 794 794
 FT CARBOHYD 67 67
 FT CARBOHYD 121 121
 FT CARBOHYD 190 190
 FT CARBOHYD 204 204
 FT CARBOHYD 255 255
 FT CARBOHYD 264 264
 FT CARBOHYD 320 320
 FT CARBOHYD 325 325
 FT CARBOHYD 341 341
 FT CARBOHYD 361 361
 FT CARBOHYD 404 404
 FT VARSPLIC 396 401
 SQ SEQUENCE 799 AA; 87868 MW; D564E8801E8978F8 CRC64;

Query Match 13.0%; Score 640.5; DB 1; Length 799;
 Best Local Similarity 29.5%; Pred. No. 5.5e-27;
 Matches 190; Conservative 78; Mismatches 155; Indels 221; Gaps 22;

QY 335 SVPLGGRVAFRLQ-----RFLPAGPWLFSISIF----- 365
 DB 289 SVHLGAAVEOHMCIPPSVDGQAPSLRWFNGS--VLNTSFLTFQLESALTNETMRH 346
 QY 366 -----SDVNNSSPALGTFP-----PAPWPPGPPPNFSSLEPR 403
 DB 347 GCLRLNQPTNVNNGNTLLAANPYGGAASIMAFMDNPEEPNEDIPISFSDVINST 406
 QY 404 GQOPVAKAASPTALLIGCLVAIIILLIILMLRWRLLSKAER-----V 454
 DB 407 SRPPEVKEDETPEGVAVAGLAVSALFL-SALL-----VLNKGQSKSGINRAV 458
 QY 455 LDEE-----LTVHLSVPGDTLLINNRGPRPPRYQEPKRNPHRACVPSNSAL---L 507
 DB 459 LAPEDGLASLHMTLGGSSL-----SPTEGKSSGLGHI 493
 QY 508 LSNFAYRLLLATYARPPRGPPPTPAMAKPTNQAVSGDYNEPEKPGAPLLPPPNQNSVP 567

DB 494 MENPOY-----FS-----DRCVH 506
 QY 568 HYAADVITLQVGTGNTYAVPALPFGAVDGGPPRVDPFPRSRLRPFKEKLGSGEGEYHLC 627
 DB 507 HIKRDIID-----LKEWELGEGAGKGYELA 530
 QY 628 E---VDSPQDLVSLDFPLNVRKGRPLVAVYKILRPDAFKNASFSLFRNDLKEVKIMSR 684
 DB 531 ECVMLNDQD-----KMLVAVALK-ETSENA-----RQDHRRAELITM 569
 QY 685 LKDNITRILLCVQVODPLCMITDYMEGNDLOFLSAHLEDKAEGAPGDAQAPPTI 744
 DB 570 LQNHIVAFEEVCCEGGGLLVAFEYMRGDLNRLRSRGPAAKLAGE---DVAEP-L 625
 QY 745 SYPMHLVAAQIASGMRYLATLNFVHDLATRNCLVGENFTIKIADFGMSRNLVAGDYR 804
 DB 626 GLGOLLVAVASQVAAAGMYALSLHFVHDLATRNCLVGGVAVKIGDGMSSHDYSTDYR 685
 QY 805 VQGRAVILPBMAMECLMGKETTASDVWARGVYLMELMCRAPQPGQLTDEVIENAG 864
 DB 686 VGGTMTLPIRMPPESITLYRKESTESDVMSFGVLMELFTYGG-QPWYQLSNTEAICL- 743
 QY 865 EFPDQGRQVYLSRPACQGLYELMLRCWSESGRPPFSQLH 908
 DB 744 -----TQGRE--LERPRACPPVYALMGCWQREPOQLSMKDVH 781
 RESULT 12
 TRKA_CHICK
 ID TRKA_CHICK STANDARD; PRT; 778 AA.
 AC 091009;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE High affinity nerve growth factor receptor precursor (EC 2.7.1.112)
 DE (Trk-A) (Fragment).
 GN TRKA.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Sympathetic ganglion;
 RX MEDLINE=97047187; PubMed=8892107;
 RA Backstrom A., Soderstrom S., Kyberg A., Ebendal T.;
 RT "Molecular cloning of the chicken trka and its expression in early
 peripheral ganglia.";
 RL J. Neurosci. Res. 46:67-81(1996).
 CC -1- FUNCTION: REQUIRED FOR HIGH-AFFINITY BINDING TO NERVE GROWTH
 CC FACTOR (NGF), NEUROTROPHIN-3 AND NEUROTROPHIN-4/5 BUT NOT BRAIN-
 CC DERIVED NEUROTROPHIC FACTOR (BDNF). KNOWN SUBSTRATES FOR THE TRK
 CC RECEPTORS ARE SHC, PI-3 KINASE, AND PLC-GAMMA-1 (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBUNIT: EXISTS IN A DYNAMIC EQUILIBRIUM BETWEEN MONOMERIC (LOW
 CC AFFINITY) AND DIMERIC (HIGH AFFINITY) STRUCTURES (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS ARE PRODUCED BY ALTERNATIVE
 CC SPLICING.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED IN THE CONDENSING DORSAL ROOT
 CC GANGLIA AT EMBRYONAL DAY 3, AND IN THE PRIMARY SYMPATHETIC CHAIN
 CC GANGLIA AT EMBRYONAL DAY 4.
 CC -1- PTM: LIGAND-MEDIATED AUTO-PHOSPHORYLATION (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
 CC PROTEIN KINASES. TRK-TYPE SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 2 LEUCINE-RICH REPEATS (LRR).
 CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
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 CC the European Bioinformatics Institute. There are no restrictions on its

RP SEQUENCE OF 378-513 FROM N.A.
RC TISSUE-Embryo;
RX MEDLINE-94084905; PubMed-8261614;
RA Williams R., Backstrom A., Ebendal T., Hallbook F.;
RT "Molecular cloning and cellular localization of trkC in the chicken embryo".
RL Brain Res. Dev. Brain Res. 75:235-252(1993).
CC -1- FUNCTION: RECEPTOR FOR NEUROTROPHIN-3 (NT-3). THIS IS A TYROSINE-
CC PROTEIN KINASE RECEPTOR. KNOWN SUBSTRATES FOR THE TRK RECEPTORS
CC ARE SHC, PI-3 KINASE, AND PLC-GAMMA-1.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- SUBUNIT: EXISTS IN A DYNAMIC EQUILIBRIUM BETWEEN MONOMERIC (LOW
CC AFFINITY) AND DIMERIC (HIGH AFFINITY) STRUCTURES.
CC -1- SUBCELLULAR LOCATION: TYPE I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: SEVERAL ISOFORMS ARE PRODUCED BY ALTERNATIVE
CC SPLICING GIVING RISE TO RECEPTORS WITH DISTINCT FUNCTIONAL
CC CAPABILITIES. THEY DIFFER IN THE EXTRACELLULAR MOTIF (ALPHA OR
CC BETA TYPES) AND/OR IN THE KINASE DOMAIN (KI, KD, KT, FL.
CC RESPECTIVELY FOR INSERTION, DELETION, TRUNCATION AND FULL LENGTH).
CC THE SEQUENCE SHOWN HERE IS THAT OF THE ALPHA/FULL LENGTH ISOFORM
CC (ALPHA/FL). THE COMBINATIONS ALPHA/FL, ALPHA/KD, AND BETA/KD HAVE
CC BEEN FOUND IN BRAIN OF A DAYS 13 AGED EMBRYO. THE KI AND KD
CC ISOFORMS FAIL TO STIMULATE TRANSFORMATION, PROCESS OUTGROWTH OR
CC SURVIVAL. THE KI ISOFORM EXHIBITS TYROSINE PHOSPHORYLATION IN THE
CC ABSENCE OF LIGAND AND IS UNABLE TO MEDIATE SURVIVAL OF NEURONAL
CC CELLS.
CC -1- DEVELOPMENTAL STAGE: EXPRESSION OCCURS IN THE EMBRYONAL DAY 2 (E2)
CC EMBRYO WITH INCREASING LEVELS LATER IN DEVELOPMENT. IN THE E9
CC EMBRYO HIGHEST LEVELS ARE FOUND IN BRAIN AND SPINAL CORD WITH
CC INTERMEDIATE LEVELS IN EYE, HEART, GUT AND MUSCLE. LOW LEVELS ARE
CC FOUND IN KIDNEY, LIVER, SKIN AND YOLK SAC.
CC -1- PTM: LIGAND-MEDIATED AUTO-PHOSPHORYLATION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES. TRK-TYPE SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 LEUCINE-RICH REPEATS (LRR).
CC -1- CAUTION: THE ADDITIONAL KINASE-DELETED ISOFORM TRK-3 WHICH
CC REPLACES THE KINASE DOMAIN WITH 19 AA INSTEAD OF 39 IN THE KD
CC ISOFORM RESULTS FROM A FRAMESHIFT.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: S74248; AAB31699.1; -
DR EMBL: X59669; CAA42202.1; -
DR EMBL: Z30091; CAA82907.1; -
DR HSSP: P11362; IEG1.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003599; Ig_MHC.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000483; LRR_Cterm.
DR InterPro: IPR000372; LRR_Nterm.
DR InterPro: IPR002011; Receptor_tyr_kin_II.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00047; Ig_1.
DR Pfam: PF00560; LRR_2.
DR Pfam: PF01463; LRRCT_1.
DR Pfam: PF01462; LRRNT_1.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR SMART: SM00082; LRRCT_1.
DR SMART: SM00409; IG_1.
DR SMART: SM00013; LRRNT_1.
DR SMART: SM00219; TYRK; 1.
DR PROSITE: PS0107; PROTEIN_KINASE_ATP_1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR_1.

DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00238; RECEPTOR_TYR_KIN_II; 1.
KW Transferase; Tyrosine-protein kinase; Transmembrane; ATP-binding;
KW Phosphorylation; Receptor; Glycoprotein; Neurogenesis; Signal;
KW Leucine-rich repeat; Repeat; Alternative splicing;
KW Immunoglobulin domain.
FT STGNL 1 31
FT CHAIN 32 827
FT DOMAIN 32 430
FT TRANSMEM 431 455
FT DOMAIN 456 827
FT REPEAT 102 125
FT REPEAT 126 149
FT DOMAIN 227 288
FT DOMAIN 319 382
FT DOMAIN 540 812
FT NP_BIND 546 554
FT BINDING 574 574
FT ACT_SITE 681 681
FT MOD_RES 518 518
FT MOD_RES 707 707
FT MOD_RES 711 711
FT MOD_RES 712 712
FT MOD_RES 822 822
FT SITE 518 518
FT SITE 822 822
FT CARBOHYD 68 68
FT CARBOHYD 72 72
FT CARBOHYD 79 79
FT CARBOHYD 163 163
FT CARBOHYD 203 203
FT CARBOHYD 218 218
FT CARBOHYD 232 232
FT CARBOHYD 259 259
FT CARBOHYD 267 267
FT CARBOHYD 272 272
FT CARBOHYD 294 294
FT CARBOHYD 375 375
FT CARBOHYD 388 388
FT VARSPPLIC 1 98
FT VARSPPLIC 581 619
FT VARSPPLIC 620 827
FT VARSPPLIC 633 664
FT VARSPPLIC 665 827
FT VARSPPLIC 713 713
FT CONFLICT 1 39
FT CONFLICT 124 124
FT CONFLICT 378 378
FT CONFLICT 481 496
FT CONFLICT 795 795
SQ SEQUENCE 827 AA; 93180 MW; AB97373113DCB28A CRC64;
Query Match 12.7%; Score 626.5; DB 1; Length 827;
Best Local Similarity 44.7%; Pred. No. 3,1e-26;
Matches 139; Conservative 50; Mismatches 81; Indels 41; Gaps 10;
OY 607 RSRLRKEKLGSGGGEVHLCEDVSDPOLVSLDFPLNVRKGGPLVYAKILRPPATKNS 666
DB 537 RSDIYLRKELGSGGAFKGYFLACYNLS-----PTNDR---MIVYAKALK-DPT----- 580
OY 667 FSLFSRNDPLKGVKIKMSRLKDPNIIRILGVCYQDDPLCITDTYMGNSDNOFLSHQLED 726
DB 581 --LAARKDQRAEELITNLQHEHYKFGVCGDGPDLVWEFYMKHGLDKFLRAH----- 634

QY 727 KAAGAP-----DGAAGCP-TISYPMILHVAQAISGKRYLATLNFVHEDLATRNCV 780
 DB 635 -----GDPAMILVGGPQROANGELGSLQMLHIAISOIASGMYVLASQHFVHDLATRNCV 689
 QY 781 GENETIKIADGSMNRNYAGDYVROGAVYPIRMAMECIMKFTTASVYAFGTYLM 840
 DB 690 GANLVKIGDGSMDYSDYVNGHMTMIPKMPPESTMYRKTSTESDVSFVILW 749
 QY 841 EVLMICRAPOGQLTDEQVIENAGEFFRDQROYLSRPACPGGLYELMCRSRESE 900
 DB 750 EIFTYGR-QPWFQSLNTEVIECI-----TQGR--VLERPRVCREYVDIMLGCMQRPQ 801
 QY 901 RPPPSQHLRL 911
 DB 802 RLNIKEIKYKIL 812

RESULT 14
 TRKC_PIG STANDARD; PRT; 825 AA.
 AC P24786;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE NT-3 growth factor receptor precursor (EC 2.7.1.112) (TRK tyrosine kinase) (GP145-TRK) (Trk-C).
 GN NTRK3 OR TRKC.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Brain;
 RX MEDLINE=91364178; PubMed=1653651;
 RA Lamballe F., Klein R., Barbacid M.
 RT "TrkC, a new member of the trk family of tyrosine protein kinases, is a receptor for neurotrophin-3".
 RL Cell 66:967-979(1991).
 CC -1- FUNCTION: RECEPTOR FOR NEUROTROPHIN-3 (NT-3). THIS IS A TYROSINE-PROTEIN KINASE RECEPTOR. KNOWN SUBSTRATES FOR THE TRK RECEPTORS ARE SHC, PI-3 KINASE, AND PLC-GAMMA-1.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.
 CC -1- SUBUNIT: EXISTS IN A DYNAMIC EQUILIBRIUM BETWEEN MONOMERIC (LOW AFFINITY) AND DIMERIC (HIGH AFFINITY) STRUCTURES.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: PREFERENTIALLY IN THE BRAIN, LOW LEVELS IN THE OVARIES.
 CC -1- PTM: LIGAND-MEDIATED AUTO-PHOSPHORYLATION.
 CC -1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-PROTEIN KINASES. TRK-TYPE SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 2 LEUCINE-RICH REPEATS (LRR).
 CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
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 CC
 CC EMBL: M80800; AAA31130.1; -
 DR PIR: A40026; A40026.
 DR HSSP: P11362; LFCK.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR003589; Ig.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR000483; LRR_Cterm.
 DR InterPro: IPR000372; LRR_Nterm.

DR InterPro: IPR002011; Receptor_tyr_kin_II.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00047; Ig; 1.
 DR Pfam: PF00560; LRR; 2.
 DR Pfam: PF01463; LRRCT; 1.
 DR Pfam: PF01462; LRRNT; 1.
 DR Pfam: PF00069; pkinase; 1.
 DR PRINTS: PR00109; TYRKINASE.
 DR SMART: SM00409; IG; 1.
 DR SMART: SM00082; LRRCT; 1.
 DR SMART: SM00013; LRRNT; 1.
 DR SMART: SM00219; TYRK; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS00239; RECEPTOR_TYR_KIN_II; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 KW Transferase; Tyrosine-protein kinase; Transmembrane; ATP-binding; Phosphorylation; Receptor; Glycoprotein; Neurogenesis; Signal; Leucine-rich repeat; Repeat; Immunoglobulin domain.
 KW Leucine-rich repeat; Repeat; Immunoglobulin domain.
 FT SIGNAL 1 31
 FT CHAIN 32 825
 FT DOMAIN 32 429
 FT TRANSMEM 430 453
 FT DOMAIN 454 825
 FT REPEAT 102 125
 FT REPEAT 126 149
 FT DOMAIN 227 288
 FT DOMAIN 319 382
 FT DOMAIN 538 814
 FT NE_BIND 544 552
 FT BINDING 572 572
 FT ACT_SITE 679 679
 FT MOD_RES 516 516
 FT MOD_RES 705 705
 FT MOD_RES 709 709
 FT MOD_RES 710 710
 FT MOD_RES 820 820
 FT SITE 516 516
 FT SITE 820 820
 FT SITE 820 820
 FT CARBOHYD 68 68
 FT CARBOHYD 72 72
 FT CARBOHYD 79 79
 FT CARBOHYD 133 133
 FT CARBOHYD 163 163
 FT CARBOHYD 203 203
 FT CARBOHYD 232 232
 FT CARBOHYD 259 259
 FT CARBOHYD 267 267
 FT CARBOHYD 272 272
 FT CARBOHYD 294 294
 FT CARBOHYD 375 375
 FT CARBOHYD 388 388
 SQ SEQUENCE 825 AA; 93129 MW; A3C671B81D28540 CRC64;

Query Match 12.7%; Score 624.5; DB 1; Length 825;
 Best Local Similarity 29.4%; Pred. No. 3; 9e-26;
 Matches 187; Conservative 85; Mismatches 175; Indels 189; Gaps 27;

QY 309 PNAW--EEGPMKHNLSGMDPRARAVSPGLGRRVRLQCFPLRAGWLLSELSFIS 366
 DB 331 PFLMLHNSQPLR-----ESKITHVEYDGEVSE--GC-----LLENKPTHYN 372
 QY 367 D---VYNNSSP-----ALGTFPPAPWPPGPPPT-NFSSL-ELFPR-----GOQPAK 410
 DB 373 NGVYTLNRQEPPLGTANQTINGHFLKEPF-----PESIDNVSYEVSPTPIVTHKPEED 428
 QY 411 AGSPAILIGCLVAITILLILLIALLMLRLMLRRLLSAERRVLEEELTVLSPGDIT 470
 DB 429 TGVSLNAGLAFACVLLVLF-----MINKYGR-----SKFGMGPA 469

QY 471 LINNPGPREPPYOE-----RPRGNPHSAPCVNPSALLSNPAVRLLATYA 521
 Db 470 VISGEEDSASLHNDOPHHHTLTGRAGHSVIGMTIP-----VINPOT----- 516
 QY 522 RPRGPGPPPTAMKPTNTQATSGDYMEPEKPGAPLLPPPPONSYPHYAADIYTLQCVT 581
 Db 517 -----FROGNCH-----KDDTYQHILKRDIV----- 539
 QY 582 GGNVAVPALPPGAVGDPFPVNDPRSRRLRKEKEIGEOPGEVHLCEVDSPODLVSLDP 641
 Db 540 -----LKEIGEGAPFKVFLAECYNLS-----P 562
 QY 642 LNVKRGHPLVAVKILRPDATKNASFSLSRNDLFKEVKINSRLKDPNILLGVCYDOD 701
 Db 563 TKV-----MLVAVALK-DPT-----LAARKDQREAEELLTNQHEHIVKFGCGGD 611
 QY 702 PLCMITDMYMGDNLNOFLSAHQLEDKAAGAPG-----DGOAAGP-TISYPMILHVAQ 755
 Db 612 PLIVFEVEMKRGDLNFKFLRAH-----GPDAMILVDGPPRAKAGELGLOMHLIASQ 662
 QY 756 IASGMRLATLNFVHRDLATNCLVGENFTIKIADFGSNRLVAGDYRYVQGRAVLPTRW 815
 Db 663 ICSGVYLASQHFVHRDLATNCLVGANLVLKIGDFGMSRDVYSTDYRYVGHTMLPIRW 722
 QY 816 MAMECIIMGKRTASDVAVRGVTLMEVILMCLRAOPFGQLTDEOVIENAGEFFRQGRVY 875
 Db 723 MPESIMVKKFTTSDVWSFVILMEIFTYRK-OPWFLSTNTEVICT-----TQGR--V 774
 QY 876 LSRRPACPOGLYELMLRCWSESEORPPFSQHLRFL 911
 Db 775 LERPRVCPEKVEYDVLGCMQOREPQRLNKEIKYIL 810

RESULT 15
 TRKC_HUMAN
 ID TRKC_HUMAN STANDARD; PRT; 839 AA.
 AC Q16288; Q16287;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE NT-3 growth factor receptor precursor (EC 2.7.1.112) (TrkC tyrosine kinase) (GPI45-TrkC) (Trk-C).
 GN NTRK3 OR TRKC.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCB1_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=95123473; PubMed=7823156;
 RA Shelton D.L., Sutherland J., Gripp J., Camerato T., Armanini M.P., Phillips H.S., Carroll K., Spencer S.D., Levinson A.D.;
 RT "Human trks: molecular cloning, tissue distribution, and expression of extracellular domain immunoadhesins.";
 RT J. Neurosci. 15:477-491(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fetal brain;
 RX MEDLINE=95104834; PubMed=7806211;
 RA McGregor L.M., Bayliss S.B., Griffin C.A., Hawkins A.L., Nelkin B.D.;
 RT "Molecular cloning of the cDNA for human TrkC (NTRK3), chromosomal assignment, and evidence for a splice variant.";
 RT Genomics 22:267-272(1994).
 CC -1- FUNCTION: RECEPTOR FOR NEUROTROPHIN-3 (NT-3). THIS IS A TYROSINE-PROTEIN KINASE RECEPTOR. KNOWN SUBSTRATES FOR THE TRK RECEPTORS ARE SHC, PI-3 KINASE, AND PLC-GAMMA-1.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine -> ADP + protein tyrosine phosphate.
 CC -1- SUBUNIT: EXISTS IN A DYNAMIC EQUILIBRIUM BETWEEN MONOMERIC (LOW AFFINITY) AND DIMERIC (HIGH AFFINITY) STRUCTURES (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.

CC -1- ALTERNATIVE PRODUCTS: AT LEAST FOUR FORMS OF TRKC ARE PRODUCED BY ALTERNATIVE SPLICING. THE DIFFERENT ISOFORMS DO NOT HAVE IDENTICAL SIGNALING PROPERTIES. THE ISOFORM B IS EXPRESSED IN A RELATIVELY LARGE AMOUNT IN THE ADULT BRAIN COMPARATIVELY TO FETAL BRAIN.
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED, MAINLY IN THE NERVOUS TISSUE.
 CC -1- PTM: LIGAND-MEDIATED AUTO-PHOSPHORYLATION.
 CC -1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-PROTEIN KINASES. TRK-TYPE SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 2 LEUCINE-RICH REPEATS (LRR).
 CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
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 CC -----
 CC EMBL: S76475; AAB3311.1; -;
 CC EMBL: S76476; AAB3311.2.1; -;
 CC EMBL: U05012; AAB75374.1; -;
 CC HSSP: P11362; IAGW.
 CC MIM: 191316; -;
 DR InterPro: IPR000719; Euk_Pkinase.
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR000483; LRR_Cterm.
 DR InterPro: IPR000372; LRR_Cterm.
 DR InterPro: IPR002011; Receptor_Tyr_kin_II.
 DR InterPro: IPR001245; Tyr_Pkinase.
 DR Pfam: PF00047; Ig_1.
 DR Pfam: PF00560; LRR_2.
 DR Pfam: PF01463; LRRT; 1.
 DR Pfam: PF01462; LRRT; 1.
 DR Pfam: PF00069; Pkinase; 1.
 DR SMART: SM00409; Ig_1.
 DR SMART: SM00082; LRRT; 1.
 DR SMART: SM00013; LRRT; 1.
 DR SMART: SM00219; TykC; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS00239; RECEPTOR_TYR_KIN_II; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 KW Transferrase; Tyrosine-protein kinase; Transmembrane; ATP-binding; Phosphorylation; Receptor; Glycoprotein; Neurogenesis; Signal;
 KW Leucine-rich repeat; Repeat; Alternative splicing;
 KW Immunoglobulin domain.
 FT SIGNAL 1 31
 FT CHAIN 32 839
 FT DOMAIN 32 429
 FT TRANSMEM 430 453
 FT DOMAIN 454 839
 FT REPEAT 102 125
 FT REPEAT 126 149
 FT DOMAIN 227 288
 FT DOMAIN 319 382
 FT DOMAIN 538 839
 FT NP_BIND 544 552
 FT BINDING 572 572
 FT ACT_SITE 679 679
 FT MOD_RES 516 516
 FT MOD_RES 705 705
 FT MOD_RES 709 709
 FT MOD_RES 710 710
 FT MOD_RES 834 834
 FT SITE 516 516
 FT SITE 834 834
 FT SITE 834 834
 FT CARBOHYD 72 72

NT-3 GROWTH FACTOR RECEPTOR.
 EXTRACELLULAR (POTENTIAL).
 POTENTIAL.
 CYTOPLASMIC (POTENTIAL).
 LRR 1.
 LRR 2.
 IG-LIKE C2-TYPE DOMAIN 1.
 IG-LIKE C2-TYPE DOMAIN 2.
 PROTEIN KINASE.
 ATP (BY SIMILARITY).
 ATP (BY SIMILARITY).
 APP (BY SIMILARITY).
 APP (BY SIMILARITY).
 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 PHOSPHORYLATION (BY SIMILARITY).
 INTERACTION WITH SHC PROTEIN (BY SIMILARITY).
 INTERACTION WITH PLC-GAMMA-1 (BY SIMILARITY).
 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 79 79 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 203 203 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 218 218 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 267 267 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 272 272 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 375 375 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 402 402 MISSING (IN ISOFORM D).
FT VARSPLIC 529 612 MISSING (IN ISOFORM D).
FT VARSPLIC 529 612 YVOHKKRDYVLRKELGAGKYLACYNLSPTKRLV
FT VARSPLIC 529 612 AVKALDPTLAARKDFOREAEELTNLOHEHYKFGYCGDG
FT VARSPLIC 529 612 HP -> YVESNIDNHGILNLDNRDHLVSTHYIEPEVO
FT VARSPLIC 529 612 SGEVSPRSHGPREIMLPISLPGHSLNNGIYEDVNI
FT VARSPLIC 529 612 PSKGRNGF (IN ISOFORM B).
FT VARSPLIC 529 612 MISSING (IN ISOFORM B).
FT VARSPLIC 529 612 MISSING (IN ISOFORM C).
FT VARSPLIC 529 612 N -> S (IN REF. 2).
FT VARSPLIC 529 612 D -> N (IN REF. 2).
SO SEQUENCE 839 AA; 94455 MM; 86D965A5003B4DD CRC64;
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Query Match 12.7%; Score 623.5; DB 1; Length 839;
Best Local Similarity 31.7%; Pred. No. 4.5e-26;
Matches 174; Conservative 67; Mismatches 131; Indels 177; Gaps 20;

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QY 490 RGNPHSACVNG-----SALLSNPA-----YRLLATYAR 522
DB 326 RGNPPTLMLNGOPLRESKIIHVEYEOGEISGCLFNKPTHYNNNGNTLI---AK 381
QY 523 PRGSGPPTPAMAKPTNTQAYSGDYME---PEKPGAPLL---PPPONSVPHVAEADIV 575
DB 382 NPLG-----TANQTINGHLKEPPESTONFILFEVSTPPTVTHKPEDETF 430
QY 576 TLQVYTGNTYAVPAL-----P 592
DB 431 GVSINAGLAFACVLLVLFVINKYGRSRKFGMKGPVAVISGEDSASPLHHNHGITT 490
QY 593 PGAVDGP-----PRVDP-----RSRLRFKELGEGOG 622
DB 491 PSSLAGPPTVIGMTIRLPIVENPOYFROGHNCHKPDYVOHKKRDYVLRKELGEGAG 550
QY 623 EYHLCVDSPODLVSLDFPLNRYKGHPLVAVKILRPATKNASFLSRNDFLKEVKIM 682
DB 551 KYFLAEC-----YNLSPTK-DKMLVAVKALK-DPT-----LAARKDFOREAEL 592
QY 683 SRLKDPNIIIRLIGVCVQDDPLCMITDYMEMGDLNQLSAHOLEDKRAGAGP----DGO 737
DB 593 TNLQHEHIVKFGYCGDDPDLIMVEYMKHGDNLKFLRAH-----GPDAMILVDOQ 643
QY 738 AAGSP-TISYPRLLNVAQAQASGMRYLATLNVRHDLATRNCLVGENFTIKIADFGSMRN 796
DB 644 PROANGELGLOMLHIAQIASGMYLLASQHFVHDLATRNCLVGANLIVKIGDFGMSRD 703
QY 797 IYAGDYR-----VOGRAVLPIFRMAAMECITLGMKFTTASDVAFVTLMEV 842
DB 704 YSTDYVYLLFNSSGNDPCICEVSGHYMLPIFRMAPESIMYRKFTTESDVMSFGVILMEI 763
QY 843 LMLCRAQPFQGLTDEQVLENAGEFFRDGROYLSRPPACPOGLYELMLKCMSRESEORP 902
DB 764 FTYGR-QPMFOLSTNEVIECI-----TQGR--VLERPRVCPREYVDVMLGCMQREPOQRL 815
QY 903 PFSQJHRFL 911
DB 816 NIKELYKITL 824
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